

SEQUENCE LISTING

<110> O'Donnell, Michael E.
Yuzhakov, Alexander
Yurieva, Olga
Jeruzalmi, David
Bruck, Irina
Kuriyan, John

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 60/143,202

<151> 1997-04-08

<150> 08/823,407

<151> 1997-04-08

<150> 09/057,416

<151> 1998-04-08

<160> 212

<170> PatentIn Ver. 2.1

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<211> 2007

<212> DNA

<213> Thermus thermophilus

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<210> 2

<211> 529

<212> PRT

<213> *Thermus thermophilus*

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Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
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Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
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Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
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Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
130 135 140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
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Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
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Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
180 185 190
Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
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Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
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Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
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 Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
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 465 470 475 480
 Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
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<211> 1590

<212> DNA

<213> *Thermus thermophilus*

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<211> 464

<212> PRT

<213> *Thermus thermophilus*

<400> 4

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      20             25             30

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Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
      35             40             45

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Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
      50             55             60

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Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
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Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
      85             90             95

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Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
100 105 110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
165 170 175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
180 185 190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
245 250 255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
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Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
275 280 285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
290 295 300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
305 310 315 320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
325 330 335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
340 345 350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365
 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380
 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400
 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415
 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
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<210> 5

<211> 454

<212> PRT

<213> Thermus thermophilus

<400> 5

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 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser

85					90					95					
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			100					105					110		
Ser	Ala	Pro	Arg	Lys	Val	Phe	Ile	Leu	Asp	Glu	Ala	His	Met	Leu	Ser
			115					120					125		
Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro
			130					135					140		
His	Val	Leu	Phe	Val	Phe	Ala	Thr	Thr	Glu	Pro	Glu	Arg	Met	Pro	Pro
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Thr	Ile	Leu	Ser	Arg	Thr	Gln	His	Phe	Arg	Phe	Arg	Arg	Leu	Thr	Glu
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Glu	Glu	Ile	Ala	Phe	Lys	Leu	Arg	Arg	Ile	Leu	Glu	Ala	Val	Gly	Arg
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Glu	Ala	Glu	Glu	Glu	Ala	Leu	Leu	Leu	Leu	Ala	Arg	Leu	Ala	Asp	Gly
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225									235						240
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Gly	Arg	Ala	Leu	Ala	Ala	Glu	Ala	Leu	Pro	Gln	Pro	Thr	Gly	Ala	Pro

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Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro		
355	360	365
Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe		
370	375	380
Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg		
385	390	395
Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys		
405	410	415
Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro		
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Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu		
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<210> 6
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 6
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32

<210> 7
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

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<210> 8
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

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<210> 9
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 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: peptide

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<210> 10
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

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<210> 11
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 <212> DNA
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 <220>
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<210> 12
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

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 <210> 13
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 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 13
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 <210> 14
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 <223> Description of Artificial Sequence: primer

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<223> Description of Artificial Sequence: primer

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<210> 17
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<210> 18
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

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<210> 19

<211> 180

<212> PRT

<213> Escherichia coli

<400> 19

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Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
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Ala Leu Asp Val
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<210> 20
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 <212> PRT
 <213> Bacillus subtilis

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 Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
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 Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
 65 70 75 80
 Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
 85 90 95
 Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
 100 105 110
 Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
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 His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
 130 135 140
 Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
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 Arg Ile Thr Ser
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<210> 21
 <211> 294
 <212> PRT

<213> Escherichia coli

<400> 21

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Ser	Leu	Gly	Arg	Ile	His	His	Ala	Tyr	Leu	Phe	Ser	Gly	Thr	Arg	Gly	
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Ser	Arg	Thr	Lys	Val	Glu	Asp	Thr	Arg	Asp	Leu	Leu	Asp	Asn	Val	Gln	
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Tyr	Ala	Pro	Ala	Arg	Gly	Arg	Phe	Lys	Val	Tyr	Leu	Ile	Asp	Glu	Val	
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Glu	Glu	His	Ile	Ala	His	Glu	Pro	Arg	Ala	Leu	Gln	Leu	Leu	Ala	Arg	
	195						200					205				
Ala	Ala	Glu	Gly	Ser	Leu	Arg	Asp	Ala	Leu	Ser	Leu	Thr	Asp	Gln	Ala	
	210					215					220					
Ile	Ala	Ser	Gly	Asp	Gly	Gln	Val	Ser	Thr	Gln	Ala	Val	Ser	Ala	Met	
225					230					235					240	

Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met
245 250 255

Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala
260 265 270

Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu
275 280 285

Leu His Arg Ile Ala Met
290

<210> 22

<211> 294

<212> PRT

<213> Haemophilus influenzae

<400> 22

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu
20 25 30

Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys
50 55 60

Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys
65 70 75 80

Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln
100 105 110

Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr
180 185 190

Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys
195 200 205

Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala
210 215 220

Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met
225 230 235 240

Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu
245 250 255

His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala
260 265 270

Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
275 280 285

Leu His Gln Ile Ala Leu
290

<210> 23
<211> 294
<212> PRT
<213> Bacillus subtilis

<400> 23
Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys

65		70		75		80									
Gly	Ile	Thr	Asn	Gly	Ser	Ile	Ser	Asp	Val	Ile	Glu	Ile	Asp	Ala	Ala
				85					90					95	
Ser	Asn	Asn	Gly	Val	Asp	Glu	Ile	Arg	Asp	Ile	Arg	Asp	Lys	Val	Lys
			100					105					110		
Phe	Ala	Pro	Ser	Ala	Val	Thr	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val
		115					120					125			
His	Met	Leu	Ser	Ile	Gly	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu
		130				135					140				
Glu	Pro	Pro	Glu	His	Cys	Ile	Phe	Ile	Leu	Ala	Thr	Thr	Glu	Pro	His
145					150					155					160
Lys	Ile	Pro	Leu	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Arg	Phe	Asp	Phe	Lys
			165					170					175		
Arg	Ile	Thr	Ser	Gln	Ala	Ile	Val	Gly	Arg	Met	Asn	Lys	Ile	Val	Asp
		180						185					190		
Ala	Glu	Gln	Leu	Gln	Val	Glu	Glu	Gly	Ser	Leu	Glu	Ile	Ile	Ala	Ser
		195					200					205			
Ala	Ala	His	Gly	Gly	Met	Arg	Asp	Ala	Leu	Ser	Leu	Leu	Asp	Gln	Ala
	210					215					220				
Ile	Ser	Phe	Ser	Gly	Asp	Ile	Leu	Lys	Val	Glu	Asp	Ala	Leu	Leu	Ile
225				230					235						240
Thr	Gly	Ala	Val	Ser	Gln	Leu	Tyr	Ile	Gly	Lys	Leu	Ala	Lys	Ser	Leu
			245					250					255		
His	Asp	Lys	Asn	Val	Ser	Asp	Ala	Leu	Glu	Thr	Leu	Asn	Glu	Leu	Leu
		260						265					270		
Gln	Gln	Gly	Lys	Asp	Pro	Ala	Lys	Leu	Ile	Glu	Asp	Met	Ile	Phe	Tyr
		275					280					285			
Phe	Arg	Asp	Met	Leu	Leu										
	290														

<210> 24
 <211> 300
 <212> PRT

<213> Caulobacter crescentus

<400> 24

Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu
1 5 10 15

Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe
20 25 30

Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly
35 40 45

Val Gly Lys Thr Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr
50 55 60

Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly
65 70 75 80

Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu
85 90 95

Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu
100 105 110

Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile
115 120 125

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu
130 135 140

Lys Thr Leu Glu Glu Pro Pro Pro His Ala Lys Phe Ile Phe Ala Thr
145 150 155 160

Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg
165 170 175

Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp
180 185 190

Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala
195 200 205

Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu
210 215 220

Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser
225 230 235 240

Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile
245 250 255

Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu
260 265 270

Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met
275 280 285

Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val
290 295 300

<210> 25

<211> 260

<212> PRT

<213> Mycoplasma genitalium

<400> 25

Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln
1 5 10 15

Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn
20 25 30

Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr
35 40 45

Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu
50 55 60

Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser
65 70 75 80

Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser
85 90 95

Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn
100 105 110

His Pro Phe Thr Phe Lys Lys Lys Val Tyr Ile Leu Asp Glu Ala His
115 120 125

Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu
130 135 140

Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Thr Glu Phe Asn Lys
145 150 155 160

Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys
165 170 175

Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys
180 185 190

Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu
195 200 205

Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala
210 215 220

Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His
225 230 235 240

Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Leu Lys Gln Phe
245 250 255

Tyr Gln Glu Ile
260

<210> 26

<211> 289

<212> PRT

<213> Thermus thermophilus

<400> 26

Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
1 5 10 15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
20 25 30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
35 40 45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
50 55 60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
65 70 75 80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
85 90 95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu

100	105	110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser		
115	120	125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro		
130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro		
145	150	155
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu		
165	170	175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg		
180	185	190
Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly		
195	200	205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu		
210	215	220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro		
225	230	235
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr		
245	250	255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala		
260	265	270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu		
275	280	285

Tyr

<210> 27

<211> 94

<212> DNA

<213> Thermus thermophilus

<400> 27

gccggaggga gaaaaaaaaa gccgagccca agggccccgcc cggccccacc ccgaagcgcc	60
cgcacccccg ggccccccga ggaggaggag aggc	94

<210> 28
<211> 11
<212> PRT
<213> Thermus thermophilus

<400> 28
Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
1 5 10

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (6)
<223> N at position 6 is either G or C

<220>
<221> unsure
<222> (12)
<223> N at position 12 is either G or C

<220>
<221> unsure
<222> (21)
<223> N at position 21 is either G or C

<400> 29
cacgcntacc tnttctccgg nac

23

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure

<222> (7)
<223> N at position 7 is either G or C

<220>
<221> unsure
<222> (10)
<223> N at position 10 is either G or C

<220>
<221> unsure
<222> (19)
<223> N at position 19 is either G or C

<220>
<221> unsure
<222> (22)
<223> N at position 22 is either G or C

<400> 30
gtgctcnggn ggctcctcnt cngtc 25

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gtgggatccg tggttctgga tctcgatgaa gaa 33

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gtgggatcca cggscststcs gagcagaag 29

<210> 33
<211> 34

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 33
 gcgggacacct caacgaggac ctctccatct tcaa 34

 <210> 34
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 34
 gcgggacacct tgctgtcsag sgtsagsgcg tcgta 35

 <210> 35
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 35
 gggaaggacc agcgcgtact cccctgctc ctaggtgtg 39

 <210> 36
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 36
 gtgtggatcc ttcttcttsc ccatsgc 27

 <210> 37
 <211> 27

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 37
 caccgattcc agtggtgcct aggtgtg 27

 <210> 38
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 38
 caacacctgg tgttccagga gcctgtgctt 30

 <210> 39
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 39
 ccagaatcgt ctgctgggtcg tag 23

 <210> 40
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 40
 agcaccctgg aggagcttc 19

 <210> 41
 <211> 19

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 41

catgtcgtac tgggtgtac

19

<210> 42

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (7)

<223> N at position 7 is A, C, G, or T

<220>

<221> unsure

<222> (8)

<223> N at position 8 is A, C, G, or T

<220>

<221> unsure

<222> (13)

<223> N at position 13 is A, C, G, or T

<220>

<221> unsure

<222> (14)

<223> N at position 14 is A, C, G, or T

<400> 42

gtsgtsnnsq acnnsqagac sacsggg

27

<210> 43

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (8)

<223> N at position 8 is A, C, G, or T

<220>

<221> unsure

<222> (9)

<223> N at position 9 is A, C, G, or T

<220>

<221> unsure

<222> (17)

<223> N at position 17 is A, C, G, or T

<220>

<221> unsure

<222> (18)

<223> N at position 18 is A, C, G, or T

<400> 43

gaasccsnng tcgaasnngg cgttgtg

27

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

cggggatcca cctcaatcac ctcggtg

27

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 45

cggggatccg ccaccttgcg gctccgggtg

30

<210> 46
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 46
gcgctctaga cgagttccca aagcgtgcgg t 31

<210> 47
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 47
cgcgctctaga tcacctgtat ccaga 25

<210> 48
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 48
gcggcgcata tggtaggtgg cctggacctg gag 33

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 49
cgcgctctaga tcacctgtat ccaga 25

<210> 50
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 50
 gtsctsgtsa agacscactt 20

 <210> 51
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 51
 sagsagsgcg ttgaasgtgt g 21

 <210> 52
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 52
 ctcgttggtg aaagtttccg tg 22

 <210> 53
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 53
 ctcgttggtg aaagtttccg tg 22

<210> 54
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 54
 tctggcaaca cgttctggag cacatcc 27

 <210> 55
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 55
 tgctggcggtt catcttcagg atg 23

 <210> 56
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 56
 catcctgaag atgaacgcca gca 23

 <210> 57
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 57
 aggttatcca caggggtcat gtgca 25

<210> 58
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
gtgtgtcata tgaacataac gggtcccaa 29

<210> 59
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
gcgcgaattc tcccttgtag aaggcttag 29

<210> 60
<211> 13
<212> PRT
<213> Thermus thermophilus

<400> 60
Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Thermus thermophilus

<400> 61
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys
1 5 10

<210> 62
<211> 8

<212> PRT
 <213> Thermus thermophilus

 <400> 62
 Phe Phe Ile Glu Ile Gln Asn His
 1 5

 <210> 63
 <211> 8
 <212> PRT
 <213> Thermus thermophilus

 <400> 63
 Tyr Asp Ala Leu Thr Leu Asp Asp
 1 5

 <210> 64
 <211> 6
 <212> PRT
 <213> Thermus thermophilus

 <400> 64
 Ala Met Gly Lys Lys Lys
 1 5

 <210> 65
 <211> 9
 <212> PRT
 <213> Thermus thermophilus

 <400> 65
 Phe Asn Lys Ser His Ser Ala Ala Tyr
 1 5

 <210> 66
 <211> 9
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: peptide

 <220>
 <221> PEPTIDE

<222> (3)
<223> Xaa at position 3 is undefined

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 66
Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 67
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (4)
<223> Xaa at position 4 is undefined

<220>
<221> PEPTIDE
<222> (7)
<223> Xaa at position 7 is undefined

<400> 67
His Asn Ala Xaa Phe Asp Xaa Gly Phe
1 5

<210> 68
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (3)
<223> Xaa at position 3 is undefined

<220>
 <221> PEPTIDE
 <222> (5)
 <223> Xaa at position 5 is undefined

 <400> 68
 Val Val Xaa Asp Xaa Glu Thr Thr Gly
 1 5

 <210> 69
 <211> 7
 <212> PRT
 <213> Thermus thermophilus

 <400> 69
 Val Leu Val Lys Thr His Leu
 1 5

 <210> 70
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: peptide

 <400> 70
 His Arg Ala Leu Tyr Asp
 1 5

 <210> 71
 <211> 7
 <212> PRT
 <213> Thermus thermophilus

 <400> 71
 His Thr Phe Asn Ala Leu Leu
 1 5

 <210> 72
 <211> 34
 <212> PRT
 <213> Escherichia coli

<400> 72

Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro
20 25 30

Val Val

<210> 73

<211> 34

<212> PRT

<213> *Vibrio cholerae*

<400> 73

Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro
20 25 30

Val Val

<210> 74

<211> 34

<212> PRT

<213> *Haemophilus influenzae*

<400> 74

Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu
1 5 10 15

Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro
20 25 30

Leu Val

<210> 75

<211> 34

<212> PRT

<213> *Rickettsia prowazekii*

<400> 75

Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
1 5 10 15

Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
20 25 30

Ile Val

<210> 76

<211> 34

<212> PRT

<213> *Helicobacter pylori*

<400> 76

Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
1 5 10 15

Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
20 25 30

Ile Ile

<210> 77

<211> 34

<212> PRT

<213> *Synechocystis* sp.

<400> 77

Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
1 5 10 15

Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
20 25 30

Ile Val

<210> 78

<211> 34

<212> PRT

<213> *Mycobacterium tuberculosis*

<400> 78

Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
20 25 30

Pro Leu

<210> 79

<211> 46

<212> PRT

<213> Escherichia coli

<400> 79

Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 80

<211> 46

<212> PRT

<213> Vibrio cholerae

<400> 80

Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala
1 5 10 15

Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu
35 40 45

<210> 81

<211> 46

<212> PRT

<213> Haemophilus influenzae

<400> 81

Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 82

<211> 46

<212> PRT

<213> Rickettsia prowazekii

<400> 82

Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp
1 5 10 15

Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys
20 25 30

Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp
35 40 45

<210> 83

<211> 45

<212> PRT

<213> Helicobacter pylori

<400> 83

Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser
1 5 10 15

Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp
20 25 30

Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln
35 40 45

<210> 84

<211> 46

<212> PRT

<213> Synechocystis sp.

<400> 84

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys
1 5 10 15

Leu Pro Asp Asp Val Lys Lys Thr His Lys Leu Leu Glu Ala Gly Asp
20 25 30

Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln
35 40 45

<210> 85

<211> 46

<212> PRT

<213> Mycobacterium tuberculosis

<400> 85

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
1 5 10 15

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<210> 86

<211> 3729

<212> DNA

<213> Thermus thermophilus

<400> 86

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3729

<210> 87

<211> 1245

<212> PRT

<213> *Thermus thermophilus*

<400> 87

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Ser	Leu	Leu	Asp	Gly	Ala	Pro	Lys	Leu	Ser	Asp	Leu	Leu	Lys	Trp	Val
			20				25						30		

Glu	Glu	Thr	Thr	Pro	Glu	Asp	Pro	Ala	Leu	Ala	Met	Thr	Asp	His	Gly
		35					40					45			

Asn	Leu	Phe	Gly	Ala	Val	Glu	Phe	Tyr	Lys	Lys	Ala	Thr	Glu	Met	Gly
	50					55					60				

Ile	Lys	Pro	Ile	Leu	Gly	Tyr	Glu	Ala	Tyr	Val	Ala	Ala	Glu	Ser	Arg
65					70					75					80

Phe	Asp	Arg	Lys	Arg	Gly	Lys	Gly	Leu	Asp	Gly	Gly	Tyr	Phe	His	Leu
			85					90						95	

Thr	Leu	Leu	Ala	Lys	Asp	Phe	Thr	Gly	Tyr	Gln	Asn	Leu	Val	Arg	Leu
			100					105					110		

Ala	Ser	Arg	Ala	Tyr	Leu	Glu	Gly	Phe	Tyr	Glu	Lys	Pro	Arg	Ile	Asp
		115					120					125			

Arg	Glu	Ile	Leu	Arg	Glu	His	Ala	Glu	Gly	Leu	Ile	Ala	Leu	Ser	Gly
	130					135					140				

Cys	Leu	Gly	Ala	Glu	Ile	Pro	Gln	Phe	Ile	Leu	Gln	Asp	Arg	Leu	Asp
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Leu	Ala	Glu	Ala	Arg	Leu	Asn	Glu	Tyr	Leu	Ser	Ile	Phe	Lys	Asp	Arg
				165					170					175	

Phe	Phe	Ile	Glu	Ile	Gln	Asn	His	Gly	Leu	Pro	Glu	Gln	Lys	Lys	Val
			180					185						190	

Asn	Glu	Val	Leu	Lys	Glu	Phe	Ala	Arg	Lys	Tyr	Gly	Leu	Gly	Met	Val
		195					200						205		

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His		
210	215	220
Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly		
225	230	235 240
Ala Leu Ala Leu Pro Cys Glu Glu Phe Tyr Val Lys Thr Pro Glu Glu		
245	250	255
Met Arg Ala Met Phe Pro Glu Glu Glu Val Gly Gly Arg Ser Pro Leu		
260	265	270
Thr Thr Pro Trp Arg Ser Pro His Val Gln Arg Gly Ala Ala Ile Gly		
275	280	285
Thr Arg Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Arg		
290	295	300
Thr Glu Ala Gln Tyr Leu Met Glu Leu Thr Phe Lys Gly Leu Leu Arg		
305	310	315 320
Arg Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg		
325	330	335
Leu Ser Gly Lys Leu Pro Pro His Gly Asp Gly Glu Ala Leu Ala Glu		
340	345	350
Ala Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser		
355	360	365
Leu Pro Pro Leu Ala Gly Val Lys Glu Trp Thr Ala Glu Ala Ile Phe		
370	375	380
His Arg Ala Leu Tyr Glu Leu Ser Ala Ile Glu Arg Met Gly Phe Pro		
385	390	395 400
Gly Leu Leu Pro His Arg Pro Gly Leu His Gln Leu Gly Pro Glu Lys		
405	410	415
Gly Val Ser Val Gly Pro Gly Arg Gly Gly Ala Ala Gly Ser Leu Val		
420	425	430
Ala Tyr Ala Val Gly Ile Thr Asn Ile Asp Pro Leu Arg Phe Gly Leu		
435	440	445
Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp Ile		
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Asp Thr Asp Phe Ser Asp Arg Glu Arg Asp Arg Val Ile Gln Tyr Val			
465	470	475	480
Arg Glu Arg Tyr Gly Glu Asp Lys Val Ala Gln Ile Gly Thr Leu Gly			
	485	490	495
Ser Leu Ala Ser Lys Ala Ala Leu Lys Glu Val Ala Arg Val Tyr Gly			
	500	505	510
Ile Pro Arg Lys Lys Ala Glu Glu Leu Ala Lys Leu Ile Pro Val Gln			
	515	520	525
Phe Gly Lys Pro Lys Pro Leu Gln Glu Ala Ile Gln Val Val Pro Glu			
	530	535	540
Leu Arg Ala Glu Met Glu Lys Asp Pro Lys Val Arg Glu Val Leu Glu			
545	550	555	560
Val Ala Met Arg Leu Glu Gly Leu Asn Arg His Ala Ser Val His Ala			
	565	570	575
Gly Arg Gly Gly Val Phe Ser Glu Pro Leu Thr Asp Leu Val Pro Leu			
	580	585	590
Cys Ala Thr Arg Lys Gly Gly Pro Tyr Thr Gln Tyr Asp Met Gly Ala			
	595	600	605
Val Glu Ala Leu Gly Leu Leu Lys Met Asp Phe Leu Gly Leu Arg Thr			
	610	615	620
Leu Thr Phe Leu Asp Glu Val Lys Arg Ile Val Lys Ala Ser Gln Gly			
625	630	635	640
Val Glu Leu Asp Tyr Asp Ala Leu Pro Leu Asp Asp Pro Lys Thr Phe			
	645	650	655
Ala Leu Leu Ser Arg Gly Glu Thr Lys Gly Val Phe Gln Leu Glu Ser			
	660	665	670
Gly Gly Met Thr Ala Thr Leu Arg Gly Leu Lys Pro Arg Arg Phe Glu			
	675	680	685
Asp Leu Ile Ala Ile Leu Ser Leu Tyr Arg Pro Gly Pro Met Glu His			
	690	695	700
Ile Pro Thr Tyr Ile Arg Arg His His Gly Leu Glu Pro Val Ser Tyr			
705	710	715	720

Ser Glu Phe Pro His Ala Glu Lys Tyr Leu Lys Pro Ile Leu Asp Glu
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 Thr Tyr Gly Ile Pro Val Tyr Gln Glu Gln Ile Met Gln Ile Ala Ser
 740 745 750
 Ala Val Ala Gly Tyr Ser Leu Gly Glu Ala Asp Leu Leu Arg Arg Ser
 755 760 765
 Met Gly Lys Lys Lys Val Glu Glu Met Lys Ser His Arg Glu Arg Phe
 770 775 780
 Val Gln Gly Ala Lys Glu Arg Gly Val Pro Glu Glu Glu Ala Asn Arg
 785 790 795 800
 Leu Phe Asp Met Leu Glu Ala Phe Ala Asn Tyr Gly Phe Asn Lys Ser
 805 810 815
 His Ala Ala Ala Tyr Ser Leu Leu Ser Tyr Gln Thr Ala Tyr Val Lys
 820 825 830
 Ala His Tyr Pro Val Glu Phe Met Ala Ala Leu Leu Ser Val Glu Arg
 835 840 845
 His Asp Ser Asp Lys Val Ala Glu Tyr Ile Arg Asp Ala Arg Ala Met
 850 855 860
 Gly Ile Glu Val Leu Pro Pro Asp Val Asn Arg Ser Gly Phe Asp Phe
 865 870 875 880
 Leu Val Gln Gly Arg Gln Ile Leu Phe Gly Leu Ser Ala Val Lys Asn
 885 890 895
 Val Gly Glu Ala Ala Ala Glu Ala Ile Leu Arg Glu Arg Glu Arg Gly
 900 905 910
 Gly Pro Tyr Arg Ser Leu Gly Asp Phe Leu Lys Arg Leu Asp Glu Lys
 915 920 925
 Val Leu Asn Lys Arg Thr Leu Glu Ser Leu Ile Lys Ala Gly Ala Leu
 930 935 940
 Asp Gly Phe Gly Glu Arg Ala Arg Leu Leu Ala Ser Leu Glu Gly Leu
 945 950 955 960
 Leu Lys Trp Ala Ala Glu Asn Arg Glu Lys Ala Arg Ser Gly Met Met
 965 970 975

Gly Leu Phe Ser Glu Val Glu Glu Pro Pro Leu Ala Glu Ala Ala Pro
 980 985 990
 Leu Asp Glu Ile Thr Arg Leu Arg Tyr Glu Lys Glu Ala Leu Gly Ile
 995 1000 1005
 Tyr Val Ser Gly His Pro Ile Leu Arg Tyr Pro Gly Leu Arg Glu Thr
 1010 1015 1020
 Ala Thr Cys Thr Leu Glu Glu Leu Pro His Leu Ala Arg Asp Leu Pro
 1025 1030 1035 1040
 Pro Arg Ser Arg Val Leu Leu Ala Gly Met Val Glu Glu Val Val Arg
 1045 1050 1055
 Lys Pro Thr Lys Ser Gly Gly Met Met Ala Arg Phe Val Leu Ser Asp
 1060 1065 1070
 Glu Thr Gly Ala Leu Glu Ala Val Ala Phe Gly Arg Ala Tyr Asp Gln
 1075 1080 1085
 Val Ser Pro Arg Leu Lys Glu Asp Thr Pro Val Leu Val Leu Ala Glu
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 Val Glu Arg Glu Glu Gly Gly Val Arg Val Leu Ala Gln Ala Val Trp
 1105 1110 1115 1120
 Thr Tyr Gln Glu Leu Glu Gln Val Pro Arg Ala Leu Glu Val Glu Val
 1125 1130 1135
 Glu Ala Ser Leu Pro Asp Asp Arg Gly Val Ala His Leu Lys Ser Leu
 1140 1145 1150
 Leu Asp Glu His Ala Gly Thr Leu Pro Leu Tyr Val Arg Val Gln Gly
 1155 1160 1165
 Ala Phe Gly Glu Ala Leu Leu Ala Leu Arg Glu Val Arg Val Gly Glu
 1170 1175 1180
 Glu Ala Leu Gly Ala Leu Glu Ala Ala Gly Phe Pro Ala Tyr Leu Leu
 1185 1190 1195 1200
 Pro Asn Arg Glu Val Ser Pro Arg Leu Thr Gly Ser Gly Gly Pro Arg
 1205 1210 1215
 Gly Arg Ala Leu Ser Thr Gly Leu Ala Leu Lys Thr Tyr Pro Ile Ala
 1220 1225 1230

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu
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<210> 88

<211> 198

<212> PRT

<213> *Thermus thermophilus*

<400> 88

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20 25 30

Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu
35 40 45

Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg Arg
50 55 60

Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg
65 70 75 80

Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro
85 90 95

Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala
100 105 110

Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro
115 120 125

Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser
130 135 140

Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu
145 150 155 160

Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg
165 170 175

Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr
180 185 190

Tyr Met Leu Thr Ser Gly
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<210> 89
 <211> 182
 <212> PRT
 <213> Deinococcus radiodurans

<220>
 <221> PEPTIDE
 <222> (79)
 <223> X at position 79 is undefined

<400> 89
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 20 25 30
 Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
 35 40 45
 Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
 50 55 60
 Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys
 65 70 75 80
 Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
 85 90 95
 Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
 100 105 110
 Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
 115 120 125
 Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
 130 135 140
 Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
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 Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
 165 170 175
 Glu Leu Leu Gly Glu Arg
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<210> 90
 <211> 201
 <212> PRT
 <213> Bacillus subtilis

<400> 90
 His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
 1 5 10 15

 Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
 20 25 30

 Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
 35 40 45

 Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
 50 55 60

 Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
 65 70 75 80

 Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
 85 90 95

 Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
 100 105 110

 Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
 115 120 125

 Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
 130 135 140

 Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
 145 150 155 160

 His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
 165 170 175

 His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
 180 185 190

 Lys Met Leu Lys Asp Ala Ala Glu Lys
 195 200

<210> 91
 <211> 188
 <212> PRT
 <213> Haemophilus influenzae

<220>
 <221> PEPTIDE
 <222> (47)
 <223> X at position 47 is undefined

<220>
 <221> PEPTIDE
 <222> (57)
 <223> X at position 57 is undefined

<400> 91
 Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly
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 Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile
 20 25 30
 Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His
 35 40 45
 Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val
 50 55 60
 His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu
 65 70 75 80
 Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile
 85 90 95
 His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys
 100 105 110
 Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr
 115 120 125
 Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp
 130 135 140
 Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His
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 Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met
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Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu
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<210> 92

<211> 189

<212> PRT

<213> Escherichia coli

<400> 92

Met Ser Thr Ala Ile Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr
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Gly Met Asn Gln Ile Gly Ala His Ser Glu Gly His Lys Ile Ile Glu
20 25 30

Ile Gly Ala Val Glu Val Val Asn Arg Arg Leu Thr Gly Asn Asn Phe
35 40 45

His Val Tyr Leu Lys Asp Arg Leu Val Asp Pro Glu Ala Phe Gly Val
50 55 60

His Gly Ile Ala Val Asp Phe Leu Leu Asp Lys Pro Thr Phe Ala Glu
65 70 75 80

Val Ala Val Glu Phe Met Asp Tyr Ile Arg Gly Ala Glu Leu Val Ile
85 90 95

His Asn Ala Ala Phe Asp Ile Gly Phe Met Asp Tyr Glu Phe Ser Leu
100 105 110

Leu Lys Arg Asp Ile Ala Lys Thr Asn Thr Phe Cys Lys Val Thr Asp
115 120 125

Ser Leu Ala Val Ala Arg Lys Met Phe Pro Gly Lys Arg Asn Ser Leu
130 135 140

Asp Ala Leu Cys Ala Arg Tyr Glu Ile Asp Asn Ser Lys Arg Thr Leu
145 150 155 160

His Gly Ala Leu Leu Asp Ala Gln Ile Leu Ala Glu Val Tyr Leu Ala
165 170 175

Met Thr Gly Gly Gln Thr Ser Met Ala Phe Ala Met Glu
180 185

<210> 93
 <211> 201
 <212> PRT
 <213> *Helicobacter pylori*

<400> 93
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 Glu Asn Leu Ile Thr Leu Lys Asn Leu Lys Thr Pro Leu Lys Asp Glu
 20 25 30
 Val Phe Ser Phe Ile Asp Leu Glu Thr Thr Gly Ser Cys Pro Ile Lys
 35 40 45
 His Glu Ile Leu Glu Ile Gly Ala Val Gln Val Lys Gly Gly Glu Ile
 50 55 60
 Ile Asn Arg Phe Glu Thr Leu Val Lys Val Lys Ser Val Pro Asp Tyr
 65 70 75 80
 Ile Ala Glu Leu Thr Gly Ile Thr Tyr Glu Asp Thr Leu Asn Ala Pro
 85 90 95
 Ser Ala His Glu Ala Leu Gln Glu Leu Arg Leu Phe Leu Gly Asn Ser
 100 105 110
 Val Phe Val Ala His Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg
 115 120 125
 Tyr Phe Val Glu Lys Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys
 130 135 140
 Thr Leu Asp Leu Ser Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu
 145 150 155 160
 Ser Phe Leu Lys Glu Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg
 165 170 175
 Ala Tyr Ala Asp Ala Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu
 180 185 190
 Leu Asn Leu Pro Ser Tyr Ile Lys Thr
 195 200

<210> 94
 <211> 630

<212> DNA

<213> *Thermus thermophilus*

<400> 94

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ctggagacca cggggcttgc cggcctggac gaggtgattg aggtgggcct cctccgcctg 180
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cgttcgtgga acctcaccgg catcccccg gaggccctgg aggaggcccc ctccctggag 300
gaggttcttg agaaggccta ccccctccgc ggcgacgcca ccttggtgat ccacaacgcc 360
gcctttgacc tgggcttcct ccgcccggcc ttggagggcc tgggctaccg cctggaaaac 420
cccgtggtgg actccctgcg cttggccaga cggggcttac caggccttag gcgctacggc 480
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gacgtggagc gcaccctcgc cgtggtgcac gaggtatact atatgcttac gtccggccgt 600
ccccgcacgc tttgggaact cgggaggtag                                     630
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<210> 95

<211> 210

<212> PRT

<213> *Thermus thermophilus*

<400> 95

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Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
  1              5              10              15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
      20              25              30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
      35              40              45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
      50              55              60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
      65              70              75              80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
      85              90              95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
      100             105             110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
      115             120             125

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp
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130	135	140
Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly		
145	150	155 160
Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His		
	165	170 175
Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val		
	180	185 190
Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly		
	195	200 205
Arg Glx		
210		
<210> 96		
<211> 461		
<212> PRT		
<213> Pseudomonas marcesans		
<400> 96		
Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn		
1	5	10 15
Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser		
	20	25 30
Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser		
	35	40 45
Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala		
	50	55 60
Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala		
	65	70 75 80
Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro		
	85	90 95
Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu		
	100	105 110
Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe		
	115	120 125

Asn	Arg	Phe	Val	Val	Gly	Pro	Asn	Ser	Arg	Met	Ala	His	Ala	Ala	Ala	130	135	140	
Met	Ala	Val	Ala	Glu	Ser	Pro	Gly	Arg	Glu	Phe	Asn	Pro	Leu	Phe	Ile	145	150	155	160
Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile	Gly	165	170	175	
His	Tyr	Arg	Leu	Glu	Ile	Asp	Pro	Gly	Ala	Lys	Val	Ser	Tyr	Val	Ser	180	185	190	
Thr	Glu	Thr	Phe	Thr	Asn	Asp	Leu	Ile	Leu	Ala	Ile	Arg	Gln	Asp	Arg	195	200	205	
Met	Gln	Ala	Phe	Arg	Asp	Arg	Tyr	Arg	Ala	Ala	Asp	Leu	Ile	Leu	Val	210	215	220	
Asp	Asp	Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu	Phe	225	230	235	240
Phe	His	Thr	Phe	Asn	Ala	Leu	His	Asp	Ala	Gly	Ser	Gln	Ile	Val	Leu	245	250	255	
Ala	Ser	Asp	Arg	Pro	Pro	Ser	Gln	Ile	Pro	Arg	Leu	Gln	Glu	Arg	Leu	260	265	270	
Met	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Val	Gln	Ala	Pro	Asp	275	280	285	
Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	His	Glu	Arg	290	295	300	
Val	Gly	Leu	Pro	Arg	Asp	Leu	Ile	Gln	Phe	Ile	Ala	Gly	Arg	Phe	Thr	305	310	315	320
Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Thr	Arg	Ala	Ile	Ala	Phe	325	330	335	
Ala	Ser	Ile	Thr	Gly	Leu	Pro	Met	Thr	Val	Asp	Ser	Ile	Ala	Pro	Met	340	345	350	
Leu	Asp	Pro	Asn	Gly	Gln	Gly	Val	Glu	Val	Thr	Pro	Lys	Gln	Val	Leu	355	360	365	
Asp	Lys	Val	Ala	Glu	Val	Phe	Lys	Val	Thr	Pro	Asp	Glu	Met	Arg	Ser	370	375	380	

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr
 385 390 395 400

Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr
 405 410 415

Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val
 420 425 430

Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys
 435 440 445

Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg
 450 455 460

<210> 97

<211> 447

<212> PRT

<213> Synechocystis sp.

<400> 97

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala
 1 5 10 15

Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val
 20 25 30

Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gln Val Glu Asn Gly
 35 40 45

Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu
 50 55 60

Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr
 65 70 75 80

Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro
 85 90 95

Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr
 100 105 110

Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala
 115 120 125

Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe
 130 135 140

Leu Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile
 145 150 155 160
 Ala His Tyr Arg Leu Glu Met Tyr Pro Asn Ala Lys Val Tyr Tyr Val
 165 170 175
 Ser Thr Glu Arg Phe Thr Asn Asp Leu Ile Thr Ala Ile Arg Gln Asp
 180 185 190
 Asn Met Glu Asp Phe Arg Ser Tyr Tyr Arg Ser Ala Asp Phe Leu Leu
 195 200 205
 Ile Asp Asp Ile Gln Phe Ile Lys Gly Lys Glu Tyr Thr Gln Glu Glu
 210 215 220
 Phe Phe His Thr Phe Asn Ser Leu His Glu Ala Gly Lys Gln Val Val
 225 230 235 240
 Val Ala Ser Asp Arg Ala Pro Gln Arg Ile Pro Gly Leu Gln Asp Arg
 245 250 255
 Leu Ile Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Ile Gln Val Pro
 260 265 270
 Asp Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu Tyr Asp
 275 280 285
 Arg Ile Arg Leu Pro Lys Glu Val Ile Glu Tyr Ile Ala Ser His Tyr
 290 295 300
 Thr Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Ala Ile Ala
 305 310 315 320
 Tyr Thr Ser Leu Ser Asn Val Ala Met Thr Val Glu Asn Ile Ala Pro
 325 330 335
 Val Leu Asn Pro Pro Val Glu Lys Val Ala Ala Ala Pro Glu Thr Ile
 340 345 350
 Ile Thr Ile Val Ala Gln His Tyr Gln Leu Lys Val Glu Glu Leu Leu
 355 360 365
 Ser Asn Ser Arg Arg Arg Glu Val Ser Leu Ala Arg Gln Val Gly Met
 370 375 380
 Tyr Leu Met Arg Gln His Thr Asp Leu Ser Leu Pro Arg Ile Gly Glu
 385 390 395 400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys
405 410 415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
435 440 445

<210> 98

<211> 446

<212> PRT

<213> Bacillus subtilis

<400> 98

Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe
115 120 125

Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr
130 135 140

Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu
145 150 155 160

Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys

165	170	175
Val Val Tyr Leu Ser Ser Glu Lys Phe Thr Asn Glu Phe Ile Asn Ser		
180	185	190
Ile Arg Asp Asn Lys Ala Val Asp Phe Arg Asn Arg Tyr Arg Asn Val		
195	200	205
Asp Val Leu Leu Ile Asp Asp Ile Gln Phe Leu Ala Gly Lys Glu Gln		
210	215	220
Thr Gln Glu Glu Phe Phe His Thr Phe Asn Thr Leu His Glu Glu Ser		
225	230	235
Lys Gln Ile Val Ile Ser Ser Asp Arg Pro Pro Lys Glu Ile Pro Thr		
245	250	255
Leu Glu Asp Arg Leu Arg Ser Arg Phe Glu Trp Gly Leu Ile Thr Asp		
260	265	270
Ile Thr Pro Pro Asp Leu Glu Thr Arg Ile Ala Ile Leu Arg Lys Lys		
275	280	285
Ala Lys Ala Glu Gly Leu Asp Ile Pro Asn Glu Val Met Leu Tyr Ile		
290	295	300
Ala Asn Gln Ile Asp Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile		
305	310	315
Arg Val Val Ala Tyr Ser Ser Leu Ile Asn Lys Asp Ile Asn Ala Asp		
325	330	335
Leu Ala Ala Glu Ala Leu Lys Asp Ile Ile Pro Ser Ser Lys Pro Lys		
340	345	350
Val Ile Thr Ile Lys Glu Ile Gln Arg Val Val Gly Gln Gln Phe Asn		
355	360	365
Ile Lys Leu Glu Asp Phe Lys Ala Lys Lys Arg Thr Lys Ser Val Ala		
370	375	380
Phe Pro Arg Gln Ile Ala Met Tyr Leu Ser Arg Glu Met Thr Asp Ser		
385	390	395
Ser Leu Pro Lys Ile Gly Glu Glu Phe Gly Gly Arg Asp His Thr Thr		
405	410	415
Val Ile His Ala His Glu Lys Ile Ser Lys Leu Leu Ala Asp Asp Glu		

420 425 430
 Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys
 435 440 445

 <210> 99
 <211> 507
 <212> PRT
 <213> Mycobacterium tuberculosis

 <400> 99
 Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val
 1 5 10 15

 Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser
 20 25 30

 Asp Ala Asn Leu Ser Ala Pro Leu Thr Pro Gln Gln Arg Ala Trp Leu
 35 40 45

 Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser
 50 55 60

 Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala
 65 70 75 80

 Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu
 85 90 95

 Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr
 100 105 110

 Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr
 115 120 125

 Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Ala Arg Gly Asp Asn Gln
 130 135 140

 His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser
 145 150 155 160

 Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr
 165 170 175

 Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Ala Leu Ala
 180 185 190

Ile Ala Glu Ala Pro Ala Arg Ala Tyr Asn Pro Leu Phe Ile Trp Gly
 195 200 205

Glu Ser Gly Leu Gly Lys Thr His Leu Leu His Ala Ala Gly Asn Tyr
 210 215 220

Ala Gln Arg Leu Phe Pro Gly Met Arg Val Lys Tyr Val Ser Thr Glu
 225 230 235 240

Glu Phe Thr Asn Asp Phe Ile Asn Ser Leu Arg Asp Asp Arg Lys Val
 245 250 255

Ala Phe Lys Arg Ser Tyr Arg Asp Val Asp Val Leu Leu Val Asp Asp
 260 265 270

Ile Gln Phe Ile Glu Gly Lys Glu Gly Ile Gln Glu Glu Phe Phe His
 275 280 285

Thr Phe Asn Thr Leu His Asn Ala Asn Lys Gln Ile Val Ile Ser Ser
 290 295 300

Asp Arg Pro Pro Lys Gln Leu Ala Thr Leu Glu Asp Arg Leu Arg Thr
 305 310 315 320

Arg Phe Glu Trp Gly Leu Ile Thr Asp Val Gln Pro Pro Glu Leu Glu
 325 330 335

Thr Arg Ile Ala Ile Leu Arg Lys Lys Ala Gln Met Glu Arg Leu Ala
 340 345 350

Val Pro Asp Asp Val Leu Glu Leu Ile Ala Ser Ser Ile Glu Arg Asn
 355 360 365

Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Val Thr Ala Phe Ala Ser
 370 375 380

Leu Asn Lys Thr Pro Ile Asp Lys Ala Leu Ala Glu Ile Val Leu Arg
 385 390 395 400

Asp Leu Ile Ala Asp Ala Asn Thr Met Gln Ile Ser Ala Ala Thr Ile
 405 410 415

Met Ala Ala Thr Ala Glu Tyr Phe Asp Thr Thr Val Glu Glu Leu Arg
 420 425 430

Gly Pro Gly Lys Thr Arg Ala Leu Ala Gln Ser Arg Gln Ile Ala Met
 435 440 445

Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln
 450 455 460

Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile
 465 470 475 480

Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu
 485 490 495

Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg
 500 505

<210> 100

<211> 446

<212> PRT

<213> Thermus thermophilus

<400> 100

Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
 1 5 10 15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
 20 25 30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
 35 40 45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
 50 55 60

Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
 65 70 75 80

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
 85 90 95

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
 100 105 110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
 115 120 125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
 130 135 140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
 145 150 155 160

Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn
165 170 175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg
180 185 190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe
195 200 205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn
210 215 220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro
225 230 235 240
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu
245 250 255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile
260 265 270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp
275 280 285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp
290 295 300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val
305 310 315 320
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro
325 330 335
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly
340 345 350
Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys
355 360 365
Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu
370 375 380
Leu Thr Pro Ala Ser Leu Pro Glu Ile Gly Gln Leu Phe Gly Gly Arg
385 390 395 400
Asp His Thr Thr Val Arg Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala
405 410 415

Gly Lys Pro Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu
420 425 430

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly
435 440 445

<210> 101

<211> 467

<212> PRT

<213> Escherichia coli

<400> 101

Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
1 5 10 15

Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu
20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu
35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr
50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr
65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala
85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser
100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr
115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly
130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Ala Arg Gln Val Ala Asp Asn
145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu
165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg

180	185	190
Lys Pro Asn Ala Lys Val Val Tyr Met His Ser Glu Arg Phe Val Gln		
195	200	205
Asp Met Val Lys Ala Leu Gln Asn Asn Ala Ile Glu Glu Phe Lys Arg		
210	215	220
Tyr Tyr Arg Ser Val Asp Ala Leu Leu Ile Asp Asp Ile Gln Phe Phe		
225	230	235
Ala Asn Lys Glu Arg Ser Gln Glu Glu Phe Phe His Thr Phe Asn Ala		
245	250	255
Leu Leu Glu Gly Asn Gln Gln Ile Ile Leu Thr Ser Asp Arg Tyr Pro		
260	265	270
Lys Glu Ile Asn Gly Val Glu Asp Arg Leu Lys Ser Arg Phe Gly Trp		
275	280	285
Gly Leu Thr Val Ala Ile Glu Pro Pro Glu Leu Glu Thr Arg Val Ala		
290	295	300
Ile Leu Met Lys Lys Ala Asp Glu Asn Asp Ile Arg Leu Pro Gly Glu		
305	310	315
Val Ala Phe Phe Ile Ala Lys Arg Leu Arg Ser Asn Val Arg Glu Leu		
325	330	335
Glu Gly Ala Leu Asn Arg Val Ile Ala Asn Ala Asn Phe Thr Gly Arg		
340	345	350
Ala Ile Thr Ile Asp Phe Val Arg Glu Ala Leu Arg Asp Leu Leu Ala		
355	360	365
Leu Gln Glu Lys Leu Val Thr Ile Asp Asn Ile Gln Lys Thr Val Ala		
370	375	380
Glu Tyr Tyr Lys Ile Lys Val Ala Asp Leu Leu Ser Lys Arg Arg Ser		
385	390	395
Arg Ser Val Ala Arg Pro Arg Gln Met Ala Met Ala Leu Ala Lys Glu		
405	410	415
Leu Thr Asn His Ser Leu Pro Glu Ile Gly Asp Ala Phe Gly Gly Arg		
420	425	430
Asp His Thr Thr Val Leu His Ala Cys Arg Lys Ile Glu Gln Leu Arg		

435		440		445
Glu Glu Ser His Asp Ile Lys	Glu Asp Phe Ser Asn Leu Ile Arg Thr			
450	455	460		
Leu Ser Ser				
465				
<210> 102				
<211> 440				
<212> PRT				
<213> <i>Thermatoga maritima</i>				
<400> 102				
Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys				
1	5	10	15	
Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly				
	20	25	30	
Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu				
	35	40	45	
Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu				
	50	55	60	
Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His				
65	70	75	80	
Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr				
	85	90	95	
Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly				
	100	105	110	
Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly				
	115	120	125	
Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr				
	130	135	140	
His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp				
145	150	155	160	
Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val				
	165	170	175	

Asp	Ser	Met	Lys	Glu	Gly	Lys	Leu	Asn	Glu	Phe	Arg	Glu	Lys	Tyr	Arg	180	185	190	
Lys	Lys	Val	Asp	Ile	Leu	Leu	Ile	Asp	Asp	Val	Gln	Phe	Leu	Ile	Gly	195	200	205	
Lys	Thr	Gly	Val	Gln	Thr	Glu	Leu	Phe	His	Thr	Phe	Asn	Glu	Leu	His	210	215	220	
Asp	Ser	Gly	Lys	Gln	Ile	Val	Ile	Cys	Ser	Asp	Arg	Glu	Pro	Gln	Lys	225	230	235	240
Leu	Ser	Glu	Phe	Gln	Asp	Arg	Leu	Val	Ser	Arg	Phe	Gln	Met	Gly	Leu	245	250	255	
Val	Ala	Lys	Leu	Glu	Pro	Pro	Asp	Glu	Glu	Thr	Arg	Lys	Ser	Ile	Ala	260	265	270	
Arg	Lys	Met	Leu	Glu	Ile	Glu	His	Gly	Glu	Leu	Pro	Glu	Glu	Val	Leu	275	280	285	
Asn	Phe	Val	Ala	Glu	Asn	Val	Asp	Asp	Asn	Leu	Arg	Arg	Leu	Arg	Gly	290	295	300	
Ala	Ile	Ile	Lys	Leu	Leu	Val	Tyr	Lys	Glu	Thr	Thr	Gly	Lys	Glu	Val	305	310	315	320
Asp	Leu	Lys	Glu	Ala	Ile	Leu	Leu	Leu	Lys	Asp	Phe	Ile	Lys	Pro	Asn	325	330	335	
Arg	Val	Lys	Ala	Met	Asp	Pro	Ile	Asp	Glu	Leu	Ile	Glu	Ile	Val	Ala	340	345	350	
Lys	Val	Thr	Gly	Val	Pro	Arg	Glu	Glu	Ile	Leu	Ser	Asn	Ser	Arg	Asn	355	360	365	
Val	Lys	Ala	Leu	Thr	Ala	Arg	Arg	Ile	Gly	Met	Tyr	Val	Ala	Lys	Asn	370	375	380	
Tyr	Leu	Lys	Ser	Ser	Leu	Arg	Thr	Ile	Ala	Glu	Lys	Phe	Asn	Arg	Ser	385	390	395	400
His	Pro	Val	Val	Val	Asp	Ser	Val	Lys	Lys	Val	Lys	Asp	Ser	Leu	Leu	405	410	415	
Lys	Gly	Asn	Lys	Gln	Leu	Lys	Ala	Leu	Ile	Asp	Glu	Val	Ile	Gly	Glu	420	425	430	

Ile Ser Arg Arg Ala Leu Ser Gly
435 440

<210> 103
<211> 457
<212> PRT
<213> Helicobacter pylori

<400> 103
Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
1 5 10 15

Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
20 25 30

Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
35 40 45

Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
50 55 60

Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
65 70 75 80

His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
85 90 95

Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
100 105 110

Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
115 120 125

Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
130 135 140

Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu
145 150 155 160

Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
165 170 175

Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
180 185 190

Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
195 200 205

Leu Leu Asp Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu
 210 215 220

Glu Phe Phe His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile
 225 230 235 240

Val Leu Ile Ser Asp Arg Ser Pro Lys Asn Ile Ala Gly Leu Glu Asp
 245 250 255

Arg Leu Lys Ser Arg Phe Glu Trp Gly Ile Thr Ala Lys Val Met Pro
 260 265 270

Pro Asp Leu Glu Thr Lys Leu Ser Ile Val Lys Gln Lys Cys Gln Leu
 275 280 285

Asn Gln Ile Thr Leu Pro Glu Glu Val Met Glu Tyr Ile Ala Gln His
 290 295 300

Ile Ser Asp Asn Ile Arg Gln Met Glu Gly Ala Ile Ile Lys Ile Ser
 305 310 315 320

Val Asn Ala Asn Leu Met Asn Ala Ser Ile Asp Leu Asn Leu Ala Lys
 325 330 335

Thr Val Leu Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu
 340 345 350

Glu Asn Ile Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser
 355 360 365

Glu Ile Lys Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys
 370 375 380

Leu Val Val Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser
 385 390 395 400

Leu Ala Gln Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met
 405 410 415

Tyr Ser Gly Val Lys Lys Met Leu Glu Glu Glu Lys Ser Pro Phe Val
 420 425 430

Leu Ser Leu Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp
 435 440 445

Lys Lys Thr Ala Phe Asn Ser Ser Glu
 450 455

<210> 104
 <211> 1305
 <212> DNA
 <213> *Thermus thermophilus*

<400> 104
 gtgtcgcacg aggccgtctg gcaacacggt ctggagcaca tccgccgcag catcaccgag 60
 gtggagtacc acacctgggt tgaaaggatc cgccccttgg ggatccggga cgggggtgctg 120
 gagctcgccg tgcccacctc ctttgccctg gactggatcc ggcgccacta cgccggcctc 180
 atccaggagg gccctcggtt cctcggggcc caggcgcccc ggtttgagct cggggtggtg 240
 cccgggggtc tagtccagga ggacatcttc cagccccgcg cgagcccccc ggcccaagct 300
 caacccgaag atacctttaa aacttcgtgg tggggcccaa caactccatg gccccacggc 360
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 accgacaatc cagccccga cctggaaacc cggatcgcca tcctgaagat gaacgccagc 840
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 atccgggagt gggaaggggc cctcatcgcg gcacgcctt tcgcctccct caacggcggt 960
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 ggagctcacg gggagcgccg caagaaggag gtggtcctcc cccggcagct cgccatgtac 1140
 ctggtgctgg agctcacccc ggcctccctg cccgagatcg accagctcaa cgacgaccgg 1200
 gaccacacca cggctcctta cgccatccag aaggtccagg agctcgcgga aagcgaccgg 1260
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<210> 105
 <211> 434
 <212> PRT
 <213> *Thermus thermophilus*

<400> 105
 Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
 1 5 10 15
 Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
 20 25 30
 Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
 35 40 45
 Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly

50		55		60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val				
65		70		75
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro				
	85		90	95
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly				
	100		105	110
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser				
	115		120	125
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu				
	130		135	140
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg				
145		150		155
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn				
	165		170	175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg				
	180		185	190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe				
	195		200	205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn				
	210		215	220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro				
225		230		235
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu				
	245		250	255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile				
	260		265	270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp				
	275		280	285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp				
	290		295	300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val				

305		310		315		320
Glu Leu Thr Arg	Ala Val Ala Ala	Lys Ala Leu Arg	His Leu Arg	Pro		
	325		330		335	
Arg Glu Leu Glu	Ala Asp Pro Leu	Glu Ile Ile Arg	Lys Ala Ala	Gly		
	340		345		350	
Pro Val Arg Pro	Glu Thr Pro Gly	Gly Ala His Gly	Glu Arg Arg	Lys		
	355		360		365	
Lys Glu Val Val	Leu Pro Arg Gln	Leu Ala Met Tyr	Leu Val Arg	Glu		
	370		375		380	
Leu Thr Pro Ala	Ser Leu Pro Glu	Ile Asp Gln Leu	Asn Asp Asp	Arg		
385		390		395		400
Asp His Thr Thr	Val Leu Tyr Ala	Ile Gln Lys Val	Gln Glu Leu	Ala		
	405		410		415	
Glu Ser Asp Arg	Glu Val Gln Gly	Leu Leu Arg Thr	Leu Arg Glu	Ala		
	420		425		430	

Cys Thr

<210> 106

<211> 1128

<212> DNA

<213> *Thermus thermophilus*

<400> 106

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gccgaggccg tcctgcacct gggcgagggg gtgttgcccc tggccctcga gggcggaagc 720
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ccccaggagt tcgcctcaa ggtccagggt gagggggagg ccctcaggga ggcggtgcgc 840
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cggatcctcc tctccgccga gggggactac ggcaaggggc aggaggaggt gcccgccag 960
 gtggaggggc cggacatggc cgtggcctac aacgcccgt acctcctcga ggccctcgcc 1020
 cccgtggggg accgggcca cctgggcac tccgggcca cgagcccag cctcatctgg 1080
 ggggacgggg aggggtaccg ggcggtggtg gtgccctca gggctag 1128

<210> 107

<211> 376

<212> PRT

<213> *Thermus thermophilus*

<400> 107

Met	Asn	Ile	Thr	Val	Pro	Lys	Lys	Leu	Leu	Ser	Asp	Gln	Leu	Ser	Leu
1				5				10					15		
Leu	Glu	Arg	Ile	Val	Pro	Ser	Arg	Ser	Ala	Asn	Pro	Leu	Tyr	Thr	Tyr
			20					25					30		
Leu	Gly	Leu	Tyr	Ala	Glu	Glu	Gly	Ala	Leu	Ile	Leu	Phe	Gly	Thr	Asn
		35						40					45		
Gly	Glu	Val	Asp	Leu	Glu	Val	Arg	Leu	Pro	Ala	Glu	Ala	Gln	Ser	Leu
	50						55					60			
Pro	Arg	Val	Leu	Val	Pro	Ala	Gln	Pro	Phe	Phe	Gln	Leu	Val	Arg	Ser
65					70					75					80
Leu	Pro	Gly	Asp	Leu	Val	Ala	Leu	Gly	Leu	Ala	Ser	Glu	Pro	Gly	Gln
				85					90					95	
Gly	Gly	Gln	Leu	Glu	Leu	Ser	Ser	Gly	Arg	Phe	Arg	Thr	Arg	Leu	Ser
		100						105					110		
Leu	Ala	Pro	Ala	Glu	Gly	Tyr	Pro	Glu	Leu	Leu	Val	Pro	Glu	Gly	Glu
		115					120					125			
Asp	Lys	Gly	Ala	Phe	Pro	Leu	Arg	Thr	Arg	Met	Pro	Ser	Gly	Glu	Leu
	130					135					140				
Val	Lys	Ala	Leu	Thr	His	Val	Arg	Tyr	Ala	Ala	Ser	Asn	Glu	Glu	Tyr
145					150					155				160	
Arg	Ala	Ile	Phe	Arg	Gly	Val	Gln	Leu	Glu	Phe	Ser	Pro	Gln	Gly	Phe
				165					170					175	
Arg	Ala	Val	Ala	Ser	Asp	Gly	Tyr	Arg	Leu	Ala	Leu	Tyr	Asp	Leu	Pro
		180						185					190		

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
195 200 205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
210 215 220

Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
225 230 235 240

Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
245 250 255

Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
260 265 270

Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
275 280 285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
355 360 365

Val Val Val Pro Leu Arg Val Glx
370 375

<210> 108

<211> 376

<212> PRT

<213> Thermus thermophilus

<400> 108

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
 35 40 45
 Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
 50 55 60
 Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
 65 70 75 80
 Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
 85 90 95
 Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
 100 105 110
 Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
 115 120 125
 Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
 130 135 140
 Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
 145 150 155 160
 Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
 165 170 175
 Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
 180 185 190
 Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
 195 200 205
 Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
 210 215 220
 Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
 225 230 235 240
 Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
 245 250 255
 Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
 260 265 270
 Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
 275 280 285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
 290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365

Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 109

<211> 367

<212> PRT

<213> Escherichia coli

<400> 109

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
 20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
 50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
 65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
 85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
 100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe

115	120	125
Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe		
130	135	140
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe		
145	150	155
Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg		
165	170	175
Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser		
180	185	190
Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp		
195	200	205
Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg		
210	215	220
Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg		
225	230	235
Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu		
245	250	255
Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile		
260	265	270
Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn		
275	280	285
Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu		
290	295	300
Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn		
305	310	315
Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val		
325	330	335
Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala		
340	345	350
Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu Glx		
355	360	365

<210> 110
 <211> 367
 <212> PRT
 <213> Proteus mirabilis

<400> 110
 Met Lys Phe Ile Ile Glu Arg Glu Gln Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15
 Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
 20 25 30
 Leu Leu Leu Lys Val Thr Glu Asn Thr Leu Ser Leu Thr Gly Thr Asp
 35 40 45
 Leu Glu Met Glu Met Met Ala Arg Val Ser Leu Ser Gln Ser His Glu
 50 55 60
 Ile Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Trp Arg
 65 70 75 80
 Gly Leu Pro Glu Gly Ala Glu Ile Ser Val Glu Leu Asp Gly Asp Arg
 85 90 95
 Leu Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
 100 105 110
 Ala Ser Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
 115 120 125
 Thr Leu Pro Gln Ala Thr Leu Lys Arg Leu Ile Glu Ser Thr Gln Phe
 130 135 140
 Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
 145 150 155 160
 Glu Thr Glu Asn Thr Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
 165 170 175
 Leu Ala Val Cys Ala Met Asp Ile Gly Gln Ser Leu Pro Gly His Ser
 180 185 190
 Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Leu Leu Asp
 195 200 205
 Gly Ser Gly Glu Ser Leu Leu Gln Leu Gln Ile Gly Ser Asn Asn Leu
 210 215 220

Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly
 225 230 235 240

Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr
 245 250 255

Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala
 260 265 270

Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn
 275 280 285

Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
 290 295 300

Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe
 305 310 315 320

Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu
 325 330 335

Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn
 340 345 350

Val Ala Ser Ala Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu
 355 360 365

<210> 111
 <211> 366
 <212> PRT
 <213> Haemophilus influenzae

<400> 111
 Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15

Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn
 20 25 30

Val Leu Leu Gln Ile Glu Asp Tyr Arg Leu Thr Ile Thr Gly Thr Asp
 35 40 45

Leu Glu Val Glu Leu Ser Ser Gln Thr Gln Leu Ser Ser Ser Ser Glu
 50 55 60

Asn Gly Thr Phe Thr Ile Pro Ala Lys Lys Phe Leu Asp Ile Cys Arg
 65 70 75 80

Thr	Leu	Ser	Asp	Asp	Ser	Glu	Ile	Thr	Val	Thr	Phe	Glu	Gln	Asp	Arg	85	90	95	
Ala	Leu	Val	Gln	Ser	Gly	Arg	Ser	Arg	Phe	Thr	Leu	Ala	Thr	Gln	Pro	100	105	110	
Ala	Glu	Glu	Tyr	Pro	Asn	Leu	Thr	Asp	Trp	Gln	Ser	Glu	Val	Asp	Phe	115	120	125	
Glu	Leu	Pro	Gln	Asn	Thr	Leu	Arg	Arg	Leu	Ile	Glu	Ala	Thr	Gln	Phe	130	135	140	
Ser	Met	Ala	Asn	Gln	Asp	Ala	Arg	Tyr	Phe	Leu	Asn	Gly	Met	Lys	Phe	145	150	155	160
Glu	Thr	Glu	Gly	Asn	Leu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg	165	170	175	
Leu	Ala	Val	Cys	Thr	Ile	Ser	Leu	Glu	Gln	Glu	Leu	Gln	Asn	His	Ser	180	185	190	
Val	Ile	Leu	Pro	Arg	Lys	Gly	Val	Leu	Glu	Leu	Val	Arg	Leu	Leu	Glu	195	200	205	
Thr	Asn	Asp	Glu	Pro	Ala	Arg	Leu	Gln	Ile	Gly	Thr	Asn	Asn	Leu	Arg	210	215	220	
Val	His	Leu	Lys	Asn	Thr	Val	Phe	Thr	Ser	Lys	Leu	Ile	Asp	Gly	Arg	225	230	235	240
Phe	Pro	Asp	Tyr	Arg	Arg	Val	Leu	Pro	Arg	Asn	Ala	Thr	Lys	Ile	Val	245	250	255	
Glu	Gly	Asn	Trp	Glu	Met	Leu	Lys	Gln	Ala	Phe	Ala	Arg	Ala	Ser	Ile	260	265	270	
Leu	Ser	Asn	Glu	Arg	Ala	Arg	Ser	Val	Arg	Leu	Ser	Leu	Lys	Glu	Asn	275	280	285	
Gln	Leu	Lys	Ile	Thr	Ala	Ser	Asn	Thr	Glu	His	Glu	Glu	Ala	Glu	Glu	290	295	300	
Ile	Val	Asp	Val	Asn	Tyr	Asn	Gly	Glu	Glu	Leu	Glu	Val	Gly	Phe	Asn	305	310	315	320
Val	Thr	Tyr	Ile	Leu	Asp	Val	Leu	Asn	Ala	Leu	Lys	Cys	Asn	Gln	Val	325	330	335	

Arg Met Cys Leu Thr Asp Ala Phe Ser Ser Cys Leu Ile Glu Asn Cys
340 345 350

Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu
355 360 365

<210> 112
<211> 367
<212> PRT
<213> Pseudomonas putida

<400> 112
Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu
1 5 10 15

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His

Ile	Leu	Ile	Gln	Val	Glu	Asp	Gly	Thr	Leu	Ser	Leu	Thr	Thr	Thr	Asn	35	40	45	
Leu	Glu	Ile	Glu	Leu	Ile	Ser	Lys	Ile	Glu	Ile	Ile	Thr	Lys	Tyr	Ile	50	55	60	
Pro	Gly	Lys	Thr	Thr	Ile	Ser	Gly	Arg	Lys	Ile	Leu	Asn	Ile	Cys	Arg	65	70	75	80
Thr	Leu	Ser	Glu	Lys	Ser	Lys	Ile	Lys	Met	Gln	Leu	Lys	Asn	Lys	Lys	85	90	95	
Met	Tyr	Ile	Ser	Ser	Glu	Asn	Ser	Asn	Tyr	Ile	Leu	Ser	Thr	Leu	Ser	100	105	110	
Ala	Asp	Thr	Phe	Pro	Asn	His	Gln	Asn	Phe	Asp	Tyr	Ile	Ser	Lys	Phe	115	120	125	
Asp	Ile	Ser	Ser	Asn	Ile	Leu	Lys	Glu	Met	Ile	Glu	Lys	Thr	Glu	Phe	130	135	140	
Ser	Met	Gly	Lys	Gln	Asp	Val	Arg	Tyr	Tyr	Leu	Asn	Gly	Met	Leu	Leu	145	150	155	160
Glu	Lys	Lys	Asp	Lys	Phe	Leu	Arg	Ser	Val	Ala	Thr	Asp	Gly	Tyr	Arg	165	170	175	
Leu	Ala	Ile	Ser	Tyr	Thr	Gln	Leu	Lys	Lys	Asp	Ile	Asn	Phe	Phe	Ser	180	185	190	
Ile	Ile	Ile	Pro	Asn	Lys	Ala	Val	Met	Glu	Leu	Leu	Lys	Leu	Leu	Asn	195	200	205	
Thr	Gln	Pro	Gln	Leu	Leu	Asn	Ile	Leu	Ile	Gly	Ser	Asn	Ser	Ile	Arg	210	215	220	
Ile	Tyr	Thr	Lys	Asn	Leu	Ile	Phe	Thr	Thr	Gln	Leu	Ile	Glu	Gly	Glu	225	230	235	240
Tyr	Pro	Asp	Tyr	Lys	Ser	Val	Leu	Phe	Lys	Glu	Lys	Lys	Asn	Pro	Ile	245	250	255	
Ile	Thr	Asn	Ser	Ile	Leu	Leu	Lys	Lys	Ser	Leu	Leu	Arg	Val	Ala	Ile	260	265	270	
Leu	Ala	His	Glu	Lys	Phe	Cys	Gly	Ile	Glu	Ile	Lys	Ile	Glu	Asn	Gly	275	280	285	

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp
 290 295 300

Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn
 305 310 315 320

Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile
 325 330 335

Ala Leu Phe Leu Asn Lys Ser Lys Ser Ser Ile Gln Ile Glu Ala Glu
 340 345 350

Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg
 355 360 365

<210> 114
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 114
 gtgtggatcc tcgtccccct catgcgcgac caggaaggg 39

<210> 115
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 115
 gtgtggatcc gtggtgacct tagccac 27

<210> 116
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 116
ttcgtgtccg aggaccttgt ggtccacaac

30

<210> 117
<211> 3514
<212> DNA
<213> Aquifex aeolicus

<400> 117
atgagtaagg atttcgtcca ccttcacctg cacacccagt tctcactcct ggacggggct 60
ataaagatag acgagctcgt gaaaaaggca aaggagtatg gatacaaagc tgtcggaaatg 120
tcagaccacg gaaacctctt cggttcgtat aaattctaca aagccctgaa ggcggaagga 180
attaagccca taatcggcac ggaagcctac ttaccacgg gttcgagggtt tgacagaaag 240
actaaaacga gcgaggacaa cataaccgac aagtacaacc accacctcat acttatagca 300
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 <213> Aquifex aeolicus

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 35 40 45
 Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile
 50 55 60
 Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys
 65 70 75 80
 Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu
 85 90 95
 Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu

100	105	110
Ser Thr Leu Ala Tyr Lys Glu Gly Phe Tyr Tyr Lys Pro Arg Ile Asp		
115	120	125
Tyr Glu Leu Leu Glu Lys Tyr Gly Glu Gly Leu Ile Ala Leu Thr Ala		
130	135	140
Cys Leu Lys Gly Val Pro Thr Tyr Tyr Ala Ser Ile Asn Glu Val Lys		
145	150	155
Lys Ala Glu Glu Trp Val Lys Lys Phe Lys Asp Ile Phe Gly Asp Asp		
165	170	175
Leu Tyr Leu Glu Leu Gln Ala Asn Asn Ile Pro Glu Gln Glu Val Ala		
180	185	190
Asn Arg Asn Leu Ile Glu Ile Ala Lys Lys Tyr Asp Val Lys Leu Ile		
195	200	205
Ala Thr Gln Asp Ala His Tyr Leu Asn Pro Glu Asp Arg Tyr Ala His		
210	215	220
Thr Val Leu Met Ala Leu Gln Met Lys Lys Thr Ile His Glu Leu Ser		
225	230	235
Ser Gly Asn Phe Lys Cys Ser Asn Glu Asp Leu His Phe Ala Pro Pro		
245	250	255
Glu Tyr Met Trp Lys Lys Phe Glu Gly Lys Phe Glu Gly Trp Glu Lys		
260	265	270
Ala Leu Leu Asn Thr Leu Glu Val Met Glu Lys Thr Ala Asp Ser Phe		
275	280	285
Glu Ile Phe Glu Asn Ser Thr Tyr Leu Leu Pro Lys Tyr Asp Val Pro		
290	295	300
Pro Asp Lys Thr Leu Glu Glu Tyr Leu Arg Glu Leu Ala Tyr Lys Gly		
305	310	315
Leu Arg Gln Arg Ile Glu Arg Gly Gln Ala Lys Asp Thr Lys Glu Tyr		
325	330	335
Trp Glu Arg Leu Glu Tyr Glu Leu Glu Val Ile Asn Lys Met Gly Phe		
340	345	350
Ala Gly Tyr Phe Leu Ile Val Gln Asp Phe Ile Asn Trp Ala Lys Lys		

355	360	365
Asn Asp Ile Pro Val Gly	Pro Gly Arg Gly Ser	Ala Gly Gly Ser Leu
370	375	380
Val Ala Tyr Ala Ile Gly	Ile Thr Asp Val Asp	Pro Ile Lys His Gly
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Phe Leu Phe Glu Arg Phe	Leu Asn Pro Glu Arg	Val Ser Met Pro Asp
	405	410 415
Ile Asp Val Asp Phe Cys	Gln Asp Asn Arg Glu	Lys Val Ile Glu Tyr
	420	425 430
Val Arg Asn Lys Tyr Gly	His Asp Asn Val Ala	Gln Ile Ile Thr Tyr
	435	440 445
Asn Val Met Lys Ala Lys	Gln Thr Leu Arg Asp	Val Ala Arg Ala Met
	450	455 460
Gly Leu Pro Tyr Ser Thr	Ala Asp Lys Leu Ala	Lys Leu Ile Pro Gln
	465	470 475 480
Gly Asp Val Gln Gly Thr	Trp Leu Ser Leu Glu	Glu Met Tyr Lys Thr
	485	490 495
Pro Val Glu Glu Leu Leu	Gln Lys Tyr Gly Glu	His Arg Thr Asp Ile
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Glu Asp Asn Val Lys Lys	Phe Arg Gln Ile Cys	Glu Glu Ser Pro Glu
	515	520 525
Ile Lys Gln Leu Val Glu	Thr Ala Leu Lys Leu	Glu Gly Leu Thr Arg
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His Thr Ser Leu His Ala	Ala Gly Val Val Ile	Ala Pro Lys Pro Leu
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Ser Glu Leu Val Pro Leu	Tyr Tyr Asp Lys Glu	Gly Glu Val Ala Thr
	565	570 575
Gln Tyr Asp Met Val Gln	Leu Glu Glu Leu Gly	Leu Leu Lys Met Asp
	580	585 590
Phe Leu Gly Leu Lys Thr	Leu Thr Glu Leu Lys	Leu Met Lys Glu Leu
	595	600 605
Ile Lys Glu Arg His Gly	Val Asp Ile Asn Phe	Leu Glu Leu Pro Leu

610	615	620
Asp Asp Pro Lys Val Tyr Lys Leu Leu Gln Glu Gly Lys Thr Thr Gly		
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Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu Leu Leu Lys Lys Leu		
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Lys Pro Asp Ser Phe Asp Asp Ile Val Ala Val Leu Ala Leu Tyr Arg		
	660	665 670
Pro Gly Pro Leu Lys Ser Gly Leu Val Asp Thr Tyr Ile Lys Arg Lys		
	675	680 685
His Gly Lys Glu Pro Val Glu Tyr Pro Phe Pro Glu Leu Glu Pro Val		
	690	695 700
Leu Lys Glu Thr Tyr Gly Val Ile Val Tyr Gln Glu Gln Val Met Lys		
705	710	715 720
Met Ser Gln Ile Leu Ser Gly Phe Thr Pro Gly Glu Ala Asp Thr Leu		
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Asp Lys Phe Ile Gln Gly Ala Val Glu Arg Gly Tyr Pro Glu Glu Lys		
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Ile Arg Lys Leu Trp Glu Asp Ile Glu Lys Phe Ala Ser Tyr Ser Phe		
	770	775 780
Asn Lys Ser His Ser Val Ala Tyr Gly Tyr Ile Ser Tyr Trp Thr Ala		
785	790	795 800
Tyr Val Lys Ala His Tyr Pro Ala Glu Phe Phe Ala Val Lys Leu Thr		
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	820	825 830
Leu Phe Gly Phe Glu Ile Leu Pro Pro Asp Ile Asn Lys Ser Asp Val		
	835	840 845
Gly Phe Thr Ile Glu Gly Glu Asn Arg Ile Arg Phe Gly Leu Ala Arg		
850	855	860
Ile Lys Gly Val Gly Glu Glu Thr Ala Lys Ile Ile Val Glu Ala Arg		

865	870	875	880
Lys Lys Tyr Lys Gln Phe Lys Gly Leu Ala Asp Phe Ile Asn Lys Thr			
	885	890	895
Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala			
	900	905	910
Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys			
	915	920	925
Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe			
	930	935	940
Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu			
	945	950	955
Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr			
	965	970	975
Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu			
	980	985	990
Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu			
	995	1000	1005
Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu			
	1010	1015	1020
Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr			
	1025	1030	1035
Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Val Lys			
	1045	1050	1055
Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val			
	1060	1065	1070
Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr			
	1075	1080	1085
Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu			
	1090	1095	1100
Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn			
	1105	1110	1115
Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu			

1125

1130

1135

Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile
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Glu Lys Leu Gly Val Lys Val Ile Ile
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 <212> DNA
 <213> Aquifex aeolicus

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 <213> Aquifex aeolicus

<400> 120

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Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly
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Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys
      50              55              60

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Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg
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```

Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala
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Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn
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Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala
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His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
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Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp
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Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser
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Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu
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Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His
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Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala
 210 215 220

Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe
 225 230 235 240

Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu
 245 250 255

Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser
 260 265 270

Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu
 275 280 285

Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val
 290 295 300

Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu
 305 310 315 320

Ala Leu Leu Tyr Val Glu Asn Leu Ile Asn Arg Gly Lys Val Glu Ala
 325 330 335

Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser
 340 345 350

Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val
 355 360 365

Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro
 370 375 380

Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln
 385 390 395 400

Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu
 405 410 415

Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu
 420 425 430

Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu
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Gln Lys Ser Ser Gly Thr Arg Leu Phe
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 ccaagtcttc 1090

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 <212> PRT
 <213> Aquifex aeolicus

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Leu	Glu	Asn	Tyr	Leu	Val	Val	Ser	Val	Lys	Gly	Glu	Val	Glu	Glu	Glu
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Gly	Glu	Val	Cys	Val	His	Ser	Gln	Lys	Leu	Tyr	Asp	Ile	Val	Lys	Asn
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Leu	Asn	Ser	Ala	Tyr	Val	Tyr	Leu	His	Thr	Glu	Gly	Glu	Lys	Leu	Val
				85					90					95	
Ile	Thr	Gly	Gly	Lys	Ser	Thr	Tyr	Lys	Leu	Pro	Thr	Ala	Pro	Ala	Glu
		100						105					110		
Asp	Phe	Pro	Glu	Phe	Pro	Glu	Ile	Val	Glu	Gly	Gly	Glu	Thr	Leu	Ser
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Gly	Asn	Leu	Leu	Val	Asn	Gly	Ile	Glu	Lys	Val	Glu	Tyr	Ala	Ile	Ala
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Lys	Glu	Glu	Ala	Asn	Ile	Ala	Leu	Gln	Gly	Met	Tyr	Leu	Arg	Gly	Tyr
	145				150					155					160
Glu	Asp	Arg	Ile	His	Phe	Val	Gly	Ser	Asp	Gly	His	Arg	Leu	Ala	Leu
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Tyr	Glu	Pro	Leu	Gly	Glu	Phe	Ser	Lys	Glu	Leu	Leu	Ile	Pro	Arg	Lys
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Ser	Leu	Lys	Val	Leu	Lys	Lys	Leu	Ile	Thr	Gly	Ile	Glu	Asp	Val	Asn
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Ile	Glu	Lys	Ser	Glu	Asp	Glu	Ser	Phe	Ala	Tyr	Phe	Ser	Thr	Pro	Glu
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Trp	Lys	Leu	Ala	Val	Arg	Leu	Leu	Glu	Gly	Glu	Phe	Pro	Asp	Tyr	Met
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Ser	Val	Ile	Pro	Glu	Glu	Phe	Ser	Ala	Glu	Val	Leu	Phe	Glu	Thr	Glu
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Glu	Val	Leu	Lys	Val	Leu	Lys	Arg	Leu	Lys	Ala	Leu	Ser	Glu	Gly	Lys
		260						265					270		
Val	Phe	Pro	Val	Lys	Ile	Thr	Leu	Ser	Glu	Asn	Leu	Ala	Ile	Phe	Glu

275		280		285
Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu				
290		295		300
Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met				
305		310		320
Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr				
	325		330	335
Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu				
	340		345	350
Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val				
355		360		

<210> 123
 <211> 1093
 <212> DNA
 <213> Aquifex aeolicus

<400> 123
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 gaaaagtacg gggagaatta cacggttctg tgggggggatg agataagcga ggaggaattc 180
 tacactgccc tttccgagac cagtatatcc ggcggttcaa aggaaaaagc ggtggtcatt 240
 tacaacttcg gggatttcct gaagaagctc ggaaggaaga aaaaggaaaa agaaaggctt 300
 ataaaagtcc tcagaaacgt aaagagtaac tacgtattta tagtgtagca tgcgaaactc 360
 cagaaacagg aactttcttc ggaacctctg aaatccgtag cgtctttcgg cggatatagt 420
 gtagcaaaca ggctgagcaa ggagaggata aaacagctcg tccttaagaa gttcaaagaa 480
 aaagggataa acgtagaaaa cgatgccctt gaataccttc tccagctcac gggttacaac 540
 ttgatggagc tcaaacttga ggttgaaaaa ctgatagatt acgcaagtga aaagaaaatt 600
 ttaacactcg atgaggtaaa gagagtagcc ttctcagttc cagaaaaagc aaacgtattt 660
 gagttcgttg atttactcct cttaaaagat tacgaaaagg ctcttaaagt tttggactcc 720
 ctcatcttct tcggaataca cccctccag attatgaaaa tcctgtcctc ctatgctcta 780
 aaactttaca ccctcaagag gcttgaagag aaggagagg accggaataa ggcgatggaa 840
 agcgtgggaa taaagaacaa ctttctcaag atgaagttca aatcttactt aaaggcaaac 900
 tctaaagagg acttgaagaa cctaatactc tccctccaga ggatagacgc tttttctaaa 960
 ctttactttc aggacacagt gcagttgctg gggattttctt gacctcaaga ctggagaggg 1020
 aagttgtgaa aaatacttct catggtgat aatctttttt atgaagtttg cggtttgcgt 1080
 ttttcccggt tct 1093

<210> 124
 <211> 350
 <212> PRT

<213> Aquifex aeolicus

<400> 124

Val	Glu	Thr	Thr	Ile	Phe	Gln	Phe	Gln	Lys	Thr	Phe	Phe	Thr	Lys	Pro
1				5					10					15	
Pro	Lys	Glu	Arg	Val	Phe	Val	Leu	His	Gly	Glu	Glu	Gln	Tyr	Leu	Ile
			20					25					30		
Arg	Thr	Phe	Leu	Ser	Lys	Leu	Lys	Glu	Lys	Tyr	Gly	Glu	Asn	Tyr	Thr
		35					40					45			
Val	Leu	Trp	Gly	Asp	Glu	Ile	Ser	Glu	Glu	Glu	Phe	Tyr	Thr	Ala	Leu
	50					55					60				
Ser	Glu	Thr	Ser	Ile	Phe	Gly	Gly	Ser	Lys	Glu	Lys	Ala	Val	Val	Ile
65					70					75				80	
Tyr	Asn	Phe	Gly	Asp	Phe	Leu	Lys	Lys	Leu	Gly	Arg	Lys	Lys	Lys	Glu
			85						90					95	
Lys	Glu	Arg	Leu	Ile	Lys	Val	Leu	Arg	Asn	Val	Lys	Ser	Asn	Tyr	Val
			100					105					110		
Phe	Ile	Val	Tyr	Asp	Ala	Lys	Leu	Gln	Lys	Gln	Glu	Leu	Ser	Ser	Glu
		115					120					125			
Pro	Leu	Lys	Ser	Val	Ala	Ser	Phe	Gly	Gly	Ile	Val	Val	Ala	Asn	Arg
	130						135					140			
Leu	Ser	Lys	Glu	Arg	Ile	Lys	Gln	Leu	Val	Leu	Lys	Lys	Phe	Lys	Glu
145					150					155				160	
Lys	Gly	Ile	Asn	Val	Glu	Asn	Asp	Ala	Leu	Glu	Tyr	Leu	Leu	Gln	Leu
			165						170					175	
Thr	Gly	Tyr	Asn	Leu	Met	Glu	Leu	Lys	Leu	Glu	Val	Glu	Lys	Leu	Ile
			180					185					190		
Asp	Tyr	Ala	Ser	Glu	Lys	Lys	Ile	Leu	Thr	Leu	Asp	Glu	Val	Lys	Arg
		195					200					205			
Val	Ala	Phe	Ser	Val	Ser	Glu	Asn	Val	Asn	Val	Phe	Glu	Phe	Val	Asp
	210						215				220				
Leu	Leu	Leu	Leu	Lys	Asp	Tyr	Glu	Lys	Ala	Leu	Lys	Val	Leu	Asp	Ser
225					230					235				240	

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser
 245 250 255

 Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly
 260 265 270

 Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe
 275 280 285

 Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp
 290 295 300

 Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys
 305 310 315 320

 Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser
 325 330 335

 Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly
 340 345 350

<210> 125
 <211> 1051
 <212> DNA
 <213> Aquifex aeolicus

<400> 125
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 ttttacggca aagaaggaag cggaaagacg aaaacagctt ttgaatttgc aaaaggtatt 120
 ttatgtaagg aaaacgtacc tggggatgcg gaagttgtcc ctcttgcaaa cacgtaaacg 180
 agctggagga agccttcttt aaaggagaaa tagaagactt taaagtttat aagacaagga 240
 cggtaaaaag cacttcgttt accttatggg cgaacatccc gactttgtgg taataatccc 300
 gagcggacat tacataaaga tagaacagat aagggaagtt aagaactttg cctatgtgaa 360
 gccgcacta agcaggagaa aagtaattat aatagacgac gccacgcga tgacctctca 420
 ggcggcaaac gctcttttaa aggtatttga agagccacct gcggacacca cctttatctt 480
 gaccacgaac aggcgttctg caatcctgcc gactatctc tccagaactt ttcaagtgga 540
 gttcaagggc ttttcagtaa aagaggttat ggaaatagcg aaagtagacg aggaaatagc 600
 gaaactctct ggaggcagtc taaaaagggc tatcttacta aaggaaaaca aagatatcct 660
 aaacaaagta aaggaattct tggaaaacga gccgttaaaa gtttacaagc ttgcaagtga 720
 attcgaagag tgggaacctg aaaagcaaaa actcttcctt gaaattatgg aagaattggt 780
 atctcaaaaa ttgaccgaag agaaaaaaga caattacacc taccttcttg atacgatcag 840
 actctttaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgttagc 900
 cgttcaggcg gattaataaa ccgttattga ttccgtaaca tttaaacctt aatctaaatt 960
 atgagagcct ttgaaggagg tctggatagg aaaatttgaa gattagatat atagatacga 1020
 ggaagatagg aaccgtgagc ggtgtaaaag t 1051

<210> 126
 <211> 305
 <212> PRT
 <213> Aquifex aeolicus

<400> 126
 Met Glu Lys Val Phe Leu Glu Lys Leu Gln Lys Thr Leu His Ile Pro
 1 5 10 15

 Gly Gly Leu Leu Phe Tyr Gly Lys Glu Gly Ser Gly Lys Thr Lys Thr
 20 25 30

 Ala Phe Glu Phe Ala Lys Gly Ile Leu Cys Lys Glu Asn Val Pro Trp
 35 40 45

 Gly Cys Gly Ser Cys Pro Ser Cys Lys His Val Asn Glu Leu Glu Glu
 50 55 60

 Ala Phe Phe Lys Gly Glu Ile Glu Asp Phe Lys Val Tyr Lys Asp Lys
 65 70 75 80

 Asp Gly Lys Lys His Phe Val Tyr Leu Met Gly Glu His Pro Asp Phe
 85 90 95

 Val Val Ile Ile Pro Ser Gly His Tyr Ile Lys Ile Glu Gln Ile Arg
 100 105 110

 Glu Val Lys Asn Phe Ala Tyr Val Lys Pro Ala Leu Ser Arg Arg Lys
 115 120 125

 Val Ile Ile Ile Asp Asp Ala His Ala Met Thr Ser Gln Ala Ala Asn
 130 135 140

 Ala Leu Leu Lys Val Leu Glu Glu Pro Pro Ala Asp Thr Thr Phe Ile
 145 150 155 160

 Leu Thr Thr Asn Arg Arg Ser Ala Ile Leu Pro Thr Ile Leu Ser Arg
 165 170 175

 Thr Phe Gln Val Glu Phe Lys Gly Phe Ser Val Lys Glu Val Met Glu
 180 185 190

 Ile Ala Lys Val Asp Glu Glu Ile Ala Lys Leu Ser Gly Gly Ser Leu
 195 200 205

 Lys Arg Ala Ile Leu Leu Lys Glu Asn Lys Asp Ile Leu Asn Lys Val
 210 215 220

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser
 225 230 235 240

Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile
 245 250 255

Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn
 260 265 270

Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala
 275 280 285

Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala
 290 295 300

Asp
 305

<210> 127
 <211> 630
 <212> DNA
 <213> Aquifex aeolicus

<400> 127
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 gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tcctttcaat aggtgcgggt 180
 gaggttaaaa acctggaaat agacctctct aaatcttttt acgagatact caaaagtgc 240
 gagataaagg cggcggagat acatggaata accaggaag acgttgaaaa gtacggaaag 300
 gaaccaaagg aagtaatata cgactttctg aagtacataa agggaagcgt tctcgttggc 360
 tactacgtga agtttgacgt ctcaactcgtt gagaagtact ccataaagta cttccagtat 420
 ccaatcatca actacaagtt agacctgttt agtttcgtga agagagagta ccagagtggc 480
 aggagtcttg acgaccttat gaaggaactc ggtgtagaaa taagggcaag gcacaacgcc 540
 cttgaagatg cctacataac cgctcttctt ttcttaaagt acgtttaccc gaacaggggag 600
 tacagactaa aggatctccc gattttcctt 630

<210> 128
 <211> 210
 <212> PRT
 <213> Aquifex aeolicus

<400> 128
 Met Asn Phe Leu Lys Lys Phe Leu Leu Leu Arg Lys Ala Gln Lys Ser
 1 5 10 15

Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val

20	25	30
Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp		
35	40	45
Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn		
50	55	60
Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp		
65	70	75
Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu		
85	90	95
Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr		
100	105	110
Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser		
115	120	125
Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn		
130	135	140
Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly		
145	150	155
Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala		
165	170	175
Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu		
180	185	190
Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile		
195	200	205
Phe Leu		
210		

<210> 129

<211> 526

<212> DNA

<213> Aquifex aeolicus

<400> 129

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 aacggtgaat ttcaggagga aagtcacttc ttgacgtaa aggcgtacgg aaaaatggct 180

gaagactggg ctacacgctt ctcgaaagga tacctcgtac tcgtagaggg aagactctcc 240
caggaaaagt gggagaaaaga aggaaagaag ttctcaaagg tcaggataat agcggaaaac 300
gtaagattaa taaacaggcc gaaaggtgct gaacttcaag cagaagaaga ggaggaagtt 360
cctcccattg aggaggaaat tgaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420
gaagaggacg aaataccttt ttaattttga ggagggtaaa gtatggtagt gagagctcct 480
aagaagaaag tttgtatgta ctgtgaacaa aagagagagc cagatt 526

<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus

<400> 130

Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val
1 5 10 15

Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala
20 25 30

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser
35 40 45

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala
50 55 60

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser
65 70 75 80

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile
85 90 95

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu
100 105 110

Gln Ala Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu
115 120 125

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu
130 135 140

Ile Pro Phe
145

<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

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tgcatagacg agcacaagct acttttcagg gttcttacia acctctgggtc cgagtacggc 180
aataagctcg atttcgtatt aataaaggat caccttgaaa agaaaaactt actccagaaa 240
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gaagtctgca aaatagtaaa acaacgttcc gcacagaggg cgataattca actcgggtata 360
gaactcattc acaaaggaaa ggaaaacaaa gactttcaca cattaatcga ggaagccag 420
agcaggatat tttccatagc ggaaagtgtc acatctacgc agttttacca tgtgaaagac 480
gttgcggaag aagttataga actcatttat aaattcaaaa gctctgacag gctagtcacg 540
ggactcccaa gcggtttcac ggaactcgat ctaaagacga cgggattcca ccctggagac 600
ttaataatac tcgccgcaag acccggtatg gggaaaaccg cttttatgct ctccataatc 660
tacaatctcg caaaagacga gggaaaaccg tcagctgtat tttccttggg aatgagcaag 720
gaacagctcg ttatgagact cctctctatg atgtcggagg tcccactttt caagataagg 780
tctggaagta tatcgaatga agattttaaag aagcttgaag caagcgcaat agaactcgca 840
aagtacgaca tatacctcga cgacacaccc gctctcacta caacggattt aaggataagg 900
gcaagaaaagc tcagaaaagga aaaggaagtt gagttcgtgg cgggtggacta cttgcaactt 960
ctgagaccgc cagtccgaaa gagttcaaga caggaggaag tggcagaggt ttcaagaaac 1020
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atagaacagg acgcagacct aatccttttc ctccacagac ccgagtacta caagaaaaag 1200
ccaaatcccc aagagcaggg tatagcggaa gtgataatag ccaagcaaag gcaaggaccc 1260
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cttcctgaac aacctcctga agaagaggaa ctttccgaaa ttattgaaac acaggaggat 1380
gaaggattcg aagatattga cttctgaaaa ttaaggtttt ataattttat cttgggtatc 1440
cggggtagct caatcggcag agcgggtggc tg 1472
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<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

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Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala
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Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu
    20                      25                     30

Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu
    35                      40                     45

Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp
    50                      55                     60
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Phe	Val	Leu	Ile	Lys	Asp	His	Leu	Glu	Lys	Lys	Asn	Leu	Leu	Gln	Lys	
65					70					75					80	
Ile	Pro	Ile	Asp	Trp	Leu	Glu	Glu	Leu	Tyr	Glu	Glu	Ala	Val	Ser	Pro	
			85						90					95		
Asp	Thr	Leu	Glu	Glu	Val	Cys	Lys	Ile	Val	Lys	Gln	Arg	Ser	Ala	Gln	
		100						105					110			
Arg	Ala	Ile	Ile	Gln	Leu	Gly	Ile	Thr	Ser	Thr	Gln	Phe	Tyr	His	Val	
		115					120					125				
Lys	Asp	Val	Ala	Glu	Glu	Val	Ile	Glu	Leu	Ile	Tyr	Lys	Phe	Lys	Ser	
	130					135					140					
Ser	Asp	Arg	Leu	Val	Thr	Gly	Leu	Pro	Ser	Gly	Phe	Thr	Glu	Leu	Asp	
145					150					155					160	
Leu	Lys	Thr	Thr	Gly	Phe	His	Pro	Gly	Asp	Leu	Ile	Ile	Leu	Ala	Ala	
				165					170					175		
Arg	Pro	Gly	Met	Gly	Lys	Thr	Ala	Phe	Met	Leu	Ser	Ile	Ile	Tyr	Asn	
			180					185						190		
Leu	Ala	Lys	Asp	Glu	Gly	Lys	Pro	Ser	Ala	Val	Phe	Ser	Leu	Glu	Met	
		195					200					205				
Ser	Lys	Glu	Gln	Leu	Val	Met	Arg	Leu	Leu	Ser	Met	Met	Ser	Glu	Val	
	210					215					220					
Pro	Leu	Phe	Lys	Ile	Arg	Ser	Gly	Ser	Ile	Ser	Asn	Glu	Asp	Leu	Lys	
225					230					235					240	
Lys	Leu	Glu	Ala	Ser	Ala	Ile	Glu	Leu	Ala	Lys	Tyr	Asp	Ile	Tyr	Leu	
			245						250					255		
Asp	Asp	Thr	Pro	Ala	Leu	Thr	Thr	Thr	Asp	Leu	Arg	Ile	Arg	Ala	Arg	
			260					265					270			
Lys	Leu	Arg	Lys	Glu	Lys	Glu	Val	Glu	Phe	Val	Ala	Val	Asp	Tyr	Leu	
		275					280					285				
Gln	Leu	Leu	Arg	Pro	Pro	Val	Arg	Lys	Ser	Ser	Arg	Gln	Glu	Glu	Val	
		290				295					300					
Ala	Glu	Val	Ser	Arg	Asn	Leu	Lys	Ala	Leu	Ala	Lys	Glu	Leu	His	Ile	
305					310					315					320	

Pro Val Met Ala Leu Ala Gln Leu Ser Arg Glu Val Glu Lys Arg Ser
325 330 335

Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu
340 345 350

Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys
355 360 365

Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala
370 375 380

Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys
385 390 395 400

Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro
405 410 415

Glu Glu Glu Glu Leu Ser Glu Ile Ile Glu Thr Gln Glu Asp Glu Gly
420 425 430

Phe Glu Asp Ile Asp Phe
435

<210> 133

<211> 1526

<212> DNA

<213> Aquifex aeolicus

<400> 133

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gatacaccct ccttttacgt gtctccaagt aaacaaatat tcaagtgttt cggttgcgagg 180
gtaggggggag acgcgataaa gttcgtttcc ctttacgagg acatctccta ttttgaagcc 240
gcccttgaac tcgcaaaacg ctacggaaag aaattagacc ttgaaaagat atcaaaaagac 300
gaaaaggtat acgtggctct tgacagggtt tgtgatttct acaggggaaag ctttctcaaa 360
aacagagagg caagtgahta cgtaaagagt aggggaatag accctaaagt agcgaggaaag 420
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gaagaaggat ttgcgatact tgtggaaggg tactttgacc ttttgagact tttttccgag 780
ggaataagga acgttgttgc acccctcggt acagccctga cccaaaatca ggcaaaccctc 840
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gctatgaaaa gtgccattcc cctactcctc agtgcaggag tggaagttaa tcccgtttac 960
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agactgataa acagctcagg ggagctcttt gaaacgctca taaaaaccgc aagggaatac 1080
 ttagaggaga aaacgcgtga gttcaggtat tatctgggct ttatttccga tggagtaagg 1140
 cgctttgctc tggcttcgga gtttcacacc aagtacaaag ttcctatgga aattttatta 1200
 atgaaaattg aaaaaaattc tcaagaaaaa gaaattaaac tctcctttaa ggaaaaaatc 1260
 ttcctgaaag gactgataga attaaaacca aaaatagacc ttgaagtcct gaacttaagt 1320
 cctgagttaa aggaactcgc agttaacgcc ttaaaccggag aggagcattt acttccaaaa 1380
 gaagttctcg agtaccaggt ggataacttg gagaaacttt ttaacaacat ccttagggat 1440
 ttacaaaaat ctgggaaaaa gaggaagaaa agagggttga aaaatgtaaa tacttaatta 1500
 actttaataa atttttagag ttagga 1526

<210> 134
 <211> 498
 <212> PRT
 <213> Aquifex aeolicus

<400> 134
 Met Ser Ser Asp Ile Asp Glu Leu Arg Arg Glu Ile Asp Ile Val Asp
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 Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg
 20 25 30
 Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
 35 40 45
 Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
 50 55 60
 Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
 65 70 75 80
 Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
 85 90 95
 Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
 100 105 110
 Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
 115 120 125
 Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
 130 135 140
 Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
 145 150 155 160
 Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys

	165		170		175
Gly Val Tyr Arg Asp Leu Phe Leu Arg Arg Val Val Ile Pro Ile Lys					
	180		185		190
Asp Pro Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Arg Ile Val Glu					
	195		200		205
Asp Lys Ser Pro Lys Tyr Ile Asn Ser Pro Asp Ser Arg Val Phe Lys					
	210		215		220
Lys Gly Glu Asn Leu Phe Gly Leu Tyr Glu Ala Lys Glu Tyr Ile Lys					
	225		230		235
Glu Glu Gly Phe Ala Ile Leu Val Glu Gly Tyr Phe Asp Leu Leu Arg					
		245		250	255
Leu Phe Ser Glu Gly Ile Arg Asn Val Val Ala Pro Leu Gly Thr Ala					
	260		265		270
Leu Thr Gln Asn Gln Ala Asn Leu Leu Ser Lys Phe Thr Lys Lys Val					
	275		280		285
Tyr Ile Leu Tyr Asp Gly Asp Asp Ala Gly Arg Lys Ala Met Lys Ser					
	290		295		300
Ala Ile Pro Leu Leu Leu Ser Ala Gly Val Glu Val Tyr Pro Val Tyr					
	305		310		315
Leu Pro Glu Gly Tyr Asp Pro Asp Glu Phe Ile Lys Glu Phe Gly Lys					
		325		330	335
Glu Glu Leu Arg Arg Leu Ile Asn Ser Ser Gly Glu Leu Phe Glu Thr					
		340		345	350
Leu Ile Lys Thr Ala Arg Glu Asn Leu Glu Glu Lys Thr Arg Glu Phe					
	355		360		365
Arg Tyr Tyr Leu Gly Phe Ile Ser Asp Gly Val Arg Arg Phe Ala Leu					
	370		375		380
Ala Ser Glu Phe His Thr Lys Tyr Lys Val Pro Met Glu Ile Leu Leu					
	385		390		395
Met Lys Ile Glu Lys Asn Ser Gln Glu Lys Glu Ile Lys Leu Ser Phe					
		405		410	415
Lys Glu Lys Ile Phe Leu Lys Gly Leu Ile Glu Leu Lys Pro Lys Ile					

420 425 430
 Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val
 435 440 445
 Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu
 450 455 460
 Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp
 465 470 475 480
 Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val
 485 490 495
 Asn Thr

<210> 135
 <211> 705
 <212> DNA
 <213> Aquifex aeolicus

<400> 135
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 atcccaaaga ggtactggaa cgccaactta gacacttacc accccaagaa cgtatcccag 180
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 gggcttacct ttgtaggatc tcctggagtc ggcaaaactc accttgcggt tgcaacatta 300
 aaagcgattt atgagaagaa gggaatcaga ggatacttct tcgatacgaa ggatctaata 360
 ttcagggttaa aacacttaat ggacgagga aaggatacaa agttttttaa aactgtctta 420
 aactcacggg ttttggttct cgacgacctc ggttctgaga ggctcagtga ctggcagagg 480
 gaactcatct cttacataat cacttacagg tataacaacc ttaagagcac gataataacc 540
 acgaattact cactccagag ggaagaagag agtagcgtga ggataagtgc ggatcttgca 600
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 aagggttccg acctcaggaa gtctaaaaag ctatcaaccc catct 705

<210> 136
 <211> 235
 <212> PRT
 <213> Aquifex aeolicus

<400> 136
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 1 5 10 15
 Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys

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35	40	45
Asn Leu Asp Thr Tyr His Pro Lys Asn Val Ser Gln Asn Arg Ala Leu		
50	55	60
Leu Thr Ile Arg Val Phe Val His Asn Phe Asn Pro Glu Glu Gly Lys		
65	70	75
Gly Leu Thr Phe Val Gly Ser Pro Gly Val Gly Lys Thr His Leu Ala		
85	90	95
Val Ala Thr Leu Lys Ala Ile Tyr Glu Lys Lys Gly Ile Arg Gly Tyr		
100	105	110
Phe Phe Asp Thr Lys Asp Leu Ile Phe Arg Leu Lys His Leu Met Asp		
115	120	125
Glu Gly Lys Asp Thr Lys Phe Leu Lys Thr Val Leu Asn Ser Pro Val		
130	135	140
Leu Val Leu Asp Asp Leu Gly Ser Glu Arg Leu Ser Asp Trp Gln Arg		
145	150	155
Glu Leu Ile Ser Tyr Ile Ile Thr Tyr Arg Tyr Asn Asn Leu Lys Ser		
165	170	175
Thr Ile Ile Thr Thr Asn Tyr Ser Leu Gln Arg Glu Glu Glu Ser Ser		
180	185	190
Val Arg Ile Ser Ala Asp Leu Ala Ser Arg Leu Gly Glu Asn Val Val		
195	200	205
Ser Lys Ile Tyr Glu Met Asn Glu Leu Leu Val Ile Lys Gly Ser Asp		
210	215	220
Leu Arg Lys Ser Lys Lys Leu Ser Thr Pro Ser		
225	230	235

<210> 137

<211> 4101

<212> DNA

<213> *Thermatoga maritima*

<400> 137

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gtgcgtttac tggagaagaa gacgcggttt cgagtcacgt tgaacggtgt tcaaaaaagt 180
aacggggatc taaggggaaa gatactttcc cttctcaacg gtaatgtgcc ttacataaaa 240
gatgttgttt tcgaaggaaa caggctgatt ctgaaagtgc ttggagattt cgcgcgggac 300
aggatcgctt ccaaactcag aagcacgaaa aaacagctcg atgaactgct gcctcccgga 360
acagagatca tgctggaggt tgtggagcct ccggaagatc ttttgaaaaa ggaagtacca 420
caaccagaaa agagagaaga accaaagggg gaagaattga agatcgagga tgaaaaccac 480
atctttggac agaaaccag aaagatcgct ttcaccccct caaaaatctt tgagtacaac 540
aaaaagacat cgggtgaagg caagatcttc aaaatagaga agatcgaggg gaaaagaacg 600
gtccttctga tttacctgac agacggagaa gattctctga tctgcaaagt cttcaacgac 660
gttgaaaagg tcgaaggga agtatcgggt ggagacgtga tcgttgccac aggagacctc 720
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cccgcgatag ccctcacgga tcatgggaac gttcaggcca taccttactt ctacgacgcg 960
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accatgaagc gggcgtagca gatctacggt gatccgcttc ccgaaatcgt ccgaagcgt 2340
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caggagctcg ttcagaaatc tatgagcgat ggttacgtgg ttggatccag aggatccgtc 2460
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tacagggtgc cagagtgc aaactttgaa gttgtcgaag acgacagata cggagcgggt 2580
tacgaccttc ccaacaagaa ctgtccaaga tgtggggctc ctctcagaaa agacggccac 2640
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aacttctcag gagagtatca ggaacgtgct catcgttttg tggaagaact cttcggtaaa 2760
gaccacgtct atagggcggg aaccataaac accatcgcg aaagaagtgc ggtgggttac 2820
gtgagaagct acgaagagaa aaccggaaa agagctcagaa aggcggaaat ggaaagactc 2880

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atcagagcca gggaagaaaa gccgttcact tcggtggaag atctcatgaa gaggaccaag 4020
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acggaacagt tcacgctttt c 4101

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<210> 138

<211> 1367

<212> PRT

<213> *Thermatoga maritima*

<400> 138

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Met Lys Lys Ile Glu Asn Leu Lys Trp Lys Asn Val Ser Phe Lys Ser
  1             5             10             15

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```

Leu Glu Ile Asp Pro Asp Ala Gly Val Val Leu Val Ser Val Glu Lys
      20             25             30

```

```

Phe Ser Glu Glu Ile Glu Asp Leu Val Arg Leu Leu Glu Lys Lys Thr
      35             40             45

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```

Arg Phe Arg Val Ile Val Asn Gly Val Gln Lys Ser Asn Gly Asp Leu
      50             55             60

```

```

Arg Gly Lys Ile Leu Ser Leu Leu Asn Gly Asn Val Pro Tyr Ile Lys
      65             70             75             80

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Asp Val Val Phe Glu Gly Asn Arg Leu Ile Leu Lys Val Leu Gly Asp
      85             90             95

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Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Lys Gln

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100	105	110
Leu Asp Glu Leu Leu Pro Pro Gly Thr Glu Ile Met Leu Glu Val Val		
115	120	125
Glu Pro Pro Glu Asp Leu Leu Lys Lys Glu Val Pro Gln Pro Glu Lys		
130	135	140
Arg Glu Glu Pro Lys Gly Glu Glu Leu Lys Ile Glu Asp Glu Asn His		
145	150	155
Ile Phe Gly Gln Lys Pro Arg Lys Ile Val Phe Thr Pro Ser Lys Ile		
165	170	175
Phe Glu Tyr Asn Lys Lys Thr Ser Val Lys Gly Lys Ile Phe Lys Ile		
180	185	190
Glu Lys Ile Glu Gly Lys Arg Thr Val Leu Leu Ile Tyr Leu Thr Asp		
195	200	205
Gly Glu Asp Ser Leu Ile Cys Lys Val Phe Asn Asp Val Glu Lys Val		
210	215	220
Glu Gly Lys Val Ser Val Gly Asp Val Ile Val Ala Thr Gly Asp Leu		
225	230	235
Leu Leu Glu Asn Gly Glu Pro Thr Leu Tyr Val Lys Gly Ile Thr Lys		
245	250	255
Leu Pro Glu Ala Lys Arg Met Asp Lys Ser Pro Val Lys Arg Val Glu		
260	265	270
Leu His Ala His Thr Lys Phe Ser Asp Gln Asp Ala Ile Thr Asp Val		
275	280	285
Asn Glu Tyr Val Lys Arg Ala Lys Glu Trp Gly Phe Pro Ala Ile Ala		
290	295	300
Leu Thr Asp His Gly Asn Val Gln Ala Ile Pro Tyr Phe Tyr Asp Ala		
305	310	315
Ala Lys Glu Ala Gly Ile Lys Pro Ile Phe Gly Ile Glu Ala Tyr Leu		
325	330	335
Val Ser Asp Val Glu Pro Val Ile Arg Asn Leu Ser Asp Asp Ser Thr		
340	345	350
Phe Gly Asp Ala Thr Phe Val Val Leu Asp Phe Glu Thr Thr Gly Leu		

355		360		365
Asp Pro Gln Val Asp Glu Ile Ile Glu Ile Gly Ala Val Lys Ile Gln				
370		375		380
Gly Gly Gln Ile Val Asp Glu Tyr His Thr Leu Ile Lys Pro Ser Arg				
385		390		395 400
Glu Ile Ser Arg Lys Ser Ser Glu Ile Thr Gly Ile Thr Gln Glu Met				
	405		410	415
Leu Glu Asn Lys Arg Ser Ile Glu Glu Val Leu Pro Glu Phe Leu Gly				
	420		425	430
Phe Leu Glu Asp Ser Ile Ile Val Ala His Asn Ala Asn Phe Asp Tyr				
	435		440	445
Arg Phe Leu Arg Leu Trp Ile Lys Lys Val Met Gly Leu Asp Trp Glu				
	450		455	460
Arg Pro Tyr Ile Asp Thr Leu Ala Leu Ala Lys Ser Leu Leu Lys Leu				
	465		470	475 480
Arg Ser Tyr Ser Leu Asp Ser Val Val Glu Lys Leu Gly Leu Gly Pro				
	485		490	495
Phe Arg His His Arg Ala Leu Asp Asp Ala Arg Val Thr Ala Gln Val				
	500		505	510
Phe Leu Arg Phe Val Glu Met Met Lys Lys Ile Gly Ile Thr Lys Leu				
	515		520	525
Ser Glu Met Glu Lys Leu Lys Asp Thr Ile Asp Tyr Thr Ala Leu Lys				
	530		535	540
Pro Phe His Cys Thr Ile Leu Val Gln Asn Lys Lys Gly Leu Lys Asn				
	545		550	555 560
Leu Tyr Lys Leu Val Ser Asp Ser Tyr Ile Lys Tyr Phe Tyr Gly Val				
	565		570	575
Pro Arg Ile Leu Lys Ser Glu Leu Ile Glu Asn Arg Glu Gly Leu Leu				
	580		585	590
Val Gly Ser Ala Cys Ile Ser Gly Glu Leu Gly Arg Ala Ala Leu Glu				
	595		600	605
Gly Ala Ser Asp Ser Glu Leu Glu Glu Ile Ala Lys Phe Tyr Asp Tyr				

610				615				620							
Ile	Glu	Val	Met	Pro	Leu	Asp	Val	Ile	Ala	Glu	Asp	Glu	Glu	Asp	Leu
625					630					635					640
Asp	Arg	Glu	Arg	Leu	Lys	Glu	Val	Tyr	Arg	Lys	Leu	Tyr	Arg	Ile	Ala
				645					650					655	
Lys	Lys	Leu	Asn	Lys	Phe	Val	Val	Met	Thr	Gly	Asp	Val	His	Phe	Leu
			660					665					670		
Asp	Pro	Glu	Asp	Ala	Arg	Gly	Arg	Ala	Ala	Leu	Leu	Ala	Pro	Gln	Gly
		675					680					685			
Asn	Arg	Asn	Phe	Glu	Asn	Gln	Pro	Ala	Leu	Tyr	Leu	Arg	Thr	Thr	Glu
		690				695					700				
Glu	Met	Leu	Glu	Lys	Ala	Ile	Glu	Ile	Phe	Glu	Asp	Glu	Glu	Ile	Ala
705					710					715					720
Arg	Glu	Val	Val	Ile	Glu	Asn	Pro	Asn	Arg	Ile	Ala	Asp	Met	Ile	Glu
				725					730					735	
Glu	Val	Gln	Pro	Leu	Glu	Lys	Lys	Leu	His	Pro	Pro	Ile	Ile	Glu	Asn
			740					745					750		
Ala	Asp	Glu	Ile	Val	Arg	Asn	Leu	Thr	Met	Lys	Arg	Ala	Tyr	Glu	Ile
		755					760					765			
Tyr	Gly	Asp	Pro	Leu	Pro	Glu	Ile	Val	Gln	Lys	Arg	Val	Glu	Lys	Glu
	770					775					780				
Leu	Asn	Ala	Ile	Ile	Asn	His	Gly	Tyr	Ala	Val	Leu	Tyr	Leu	Ile	Ala
785					790				795						800
Gln	Glu	Leu	Val	Gln	Lys	Ser	Met	Ser	Asp	Gly	Tyr	Val	Val	Gly	Ser
				805					810					815	
Arg	Gly	Ser	Val	Gly	Ser	Ser	Leu	Val	Ala	Asn	Leu	Leu	Gly	Ile	Thr
			820					825					830		
Glu	Val	Asn	Pro	Leu	Pro	Pro	His	Tyr	Arg	Cys	Pro	Glu	Cys	Lys	Tyr
		835					840					845			
Phe	Glu	Val	Val	Glu	Asp	Asp	Arg	Tyr	Gly	Ala	Gly	Tyr	Asp	Leu	Pro
	850					855					860				
Asn	Lys	Asn	Cys	Pro	Arg	Cys	Gly	Ala	Pro	Leu	Arg	Lys	Asp	Gly	His

865		870		875		880
Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro						
	885			890		895
Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg						
	900			905		910
Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr						
	915			920		925
Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr						
	930			935		940
Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu						
945		950		955		960
Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly						
	965			970		975
Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro						
	980			985		990
Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His						
	995			1000		1005
Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu						
1010		1015		1020		
Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly						
1025		1030		1035		1040
Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile						
	1045			1050		1055
Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser						
	1060			1065		1070
Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg						
	1075			1080		1085
Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg						
	1090			1095		1100
Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg						
1105		1110		1115		1120
Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys						

1125	1130	1135
Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser		
1140	1145	1150
Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr		
1155	1160	1165
Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe		
1170	1175	1180
Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala		
1185	1190	1195
Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His		
1205	1210	1215
Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln		
1220	1225	1230
Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg		
1235	1240	1245
Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn		
1250	1255	1260
Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe		
1265	1270	1275
Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu		
1285	1290	1295
Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu		
1300	1305	1310
Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro		
1315	1320	1325
Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn		
1330	1335	1340
His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu		
1345	1350	1355
Thr Glu Gln Phe Thr Leu Phe		
1365		

<210> 139
 <211> 567
 <212> DNA
 <213> *Thermatoga maritima*

<400> 139
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 aagatctaca gaaacaaagc gtttcaactct ctctgtgaatc ccagaataag aatccctgcg 180
 ctgattcaga aagttcacgg tatcagcaac atggacatcg tggaagcgcc agacatggac 240
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 aacttcgacc tcacttttct ggatatgatg gcaaaggaaa cgggaaactt tccaataacg 360
 aatccctaca tcgacacact cgatctttca gaagagatct ttggaaggcc tcattctctc 420
 aaatggctct cggaaagact tggaataaaa accacgatac ggcaccgtgc tcttcagat 480
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 aacgaattca tacgtggaaa acggggg 567

<210> 140
 <211> 189
 <212> PRT
 <213> *Thermatoga maritima*

<400> 140
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 Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile
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 Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe
 35 40 45
 His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys
 50 55 60
 Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp
 65 70 75 80
 Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val
 85 90 95
 Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys
 100 105 110
 Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp
 115 120 125

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser
 130 135 140

Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp
 145 150 155 160

Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly
 165 170 175

Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly
 180 185

<210> 141
 <211> 1434
 <212> DNA
 <213> *Thermatoga maritima*

<400> 141
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 ttgcgcggtc cgaggggaac ggggaagact actcttgcca gaattctcgc aaaatccctg 180
 aactgtgaga acagaaaggg agttgaaccc tgcaattcct gcagagcctg cagagagata 240
 gacgagggaa ccttcatgga cgtgatagag ctcgacgcgg cctccaacag aggaatagac 300
 gagatcagaa gaatcagaga cgccgttggga tacaggccga tggaaggtaa atacaaagtc 360
 tacataatag acgaagttca catgctcacg aaagaagcct tcaacgcgct cctcaaaaca 420
 ctogaagaac ctcttccca cgtcgtgttc gtgctggcaa cgacaaacct tgagaagggt 480
 cctcccacga ttatctcgag atgtcaggtt ttcgagttca gaaacattcc cgacgagctc 540
 atcgaagaaga ggctccagga agttgcggag gctgaaggaa tagagataga cagggaagct 600
 ctgagcttca tcgcaaaaag agcctctgga ggcttgagag acgcgctcac catgctcgag 660
 caggtgtgga agttctcgga aggaaagata gatctcgaga cggtagacag ggcgctcggg 720
 ttgataccga tacaggttgt tcgcgattac gtgaacgcta tcttttctgg tgatgtgaaa 780
 agggctcttca ccgttctcga cgacgtctat tacagcggga aggactacga ggtgctcatt 840
 caggaagcag tcgaggatct ggtcgaagac ctggaaaggg agagaggggt ttaccaggtt 900
 tcagcgaacg atatagttca ggttctcaga caacttctga atcttctgag agagataaag 960
 ttgcgcgaag aaaaacgact cgtctgtaaa gtgggttcgg cttacatagc gacgaggttc 1020
 tccaccacaa acgttcagga aaacgatgtc agagaaaaaa acgataattc aaatgtacag 1080
 cagaaagaag agaagaaaga aacggtgaag gcaaaagaag aaaaacagga agacagcgag 1140
 ttcgagaaac gcttcaaaga actcatggaa gaactgaaag aaaagggcga tctctctatc 1200
 tttgtcgctc tcagcctctc agaggtgcag tttgacggag aaaaggtgat tatttctttt 1260
 gattcatcga aagctatgca ttacgagttg atgaagaaaa aactgcctga gctggaaaac 1320
 attttttcta gaaaactcgg gaaaaaagta gaagttgaac ttcgactgat gggaaaagaa 1380
 gaaacaatcg agaaggtttc tcagaagatc ctgagattgt ttgaacagga ggga 1434

<210> 142
 <211> 478
 <212> PRT

<213> *Thermatoga maritima*

<400> 142

Met	Glu	Val	Leu	Tyr	Arg	Lys	Tyr	Arg	Pro	Lys	Thr	Phe	Ser	Glu	Val	
1				5					10					15		
Val	Asn	Gln	Asp	His	Val	Lys	Lys	Ala	Ile	Ile	Gly	Ala	Ile	Gln	Lys	
			20					25					30			
Asn	Ser	Val	Ala	His	Gly	Tyr	Ile	Phe	Ala	Gly	Pro	Arg	Gly	Thr	Gly	
		35					40					45				
Lys	Thr	Thr	Leu	Ala	Arg	Ile	Leu	Ala	Lys	Ser	Leu	Asn	Cys	Glu	Asn	
	50					55					60					
Arg	Lys	Gly	Val	Glu	Pro	Cys	Asn	Ser	Cys	Arg	Ala	Cys	Arg	Glu	Ile	
65					70					75					80	
Asp	Glu	Gly	Thr	Phe	Met	Asp	Val	Ile	Glu	Leu	Asp	Ala	Ala	Ser	Asn	
				85					90					95		
Arg	Gly	Ile	Asp	Glu	Ile	Arg	Arg	Ile	Arg	Asp	Ala	Val	Gly	Tyr	Arg	
		100						105					110			
Pro	Met	Glu	Gly	Lys	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val	His	Met	
	115						120					125				
Leu	Thr	Lys	Glu	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	
	130					135					140					
Pro	Ser	His	Val	Val	Phe	Val	Leu	Ala	Thr	Thr	Asn	Leu	Glu	Lys	Val	
145					150					155					160	
Pro	Pro	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Val	Phe	Glu	Phe	Arg	Asn	Ile	
			165					170						175		
Pro	Asp	Glu	Leu	Ile	Glu	Lys	Arg	Leu	Gln	Glu	Val	Ala	Glu	Ala	Glu	
		180					185						190			
Gly	Ile	Glu	Ile	Asp	Arg	Glu	Ala	Leu	Ser	Phe	Ile	Ala	Lys	Arg	Ala	
	195						200					205				
Ser	Gly	Gly	Leu	Arg	Asp	Ala	Leu	Thr	Met	Leu	Glu	Gln	Val	Trp	Lys	
	210					215					220					
Phe	Ser	Glu	Gly	Lys	Ile	Asp	Leu	Glu	Thr	Val	His	Arg	Ala	Leu	Gly	
225					230					235					240	

Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser
 245 250 255
 Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser
 260 265 270
 Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val
 275 280 285
 Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp
 290 295 300
 Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys
 305 310 315 320
 Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile
 325 330 335
 Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu
 340 345 350
 Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr
 355 360 365
 Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg
 370 375 380
 Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile
 385 390 395 400
 Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val
 405 410 415
 Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys
 420 425 430
 Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys
 435 440 445
 Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu
 450 455 460
 Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly
 465 470 475

<210> 143

<211> 1098

<212> DNA

<213> *Thermatoga maritima*

<400> 143

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atgaaagtaa ccgtcacgac tcttgaattg aaagacaaaa taaccatcgc ctcaaaagcg 60
ctcgcaaaga aatccgtgaa acccattctt gctggatttc ttttcgaagt gaaagatgga 120
aattttctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgaggcacg ttttgtggta ccaggagatg tcattcagaa gatggtcaag 240
gttctccag atgagataac ggaactttct ttagaggggg atgctcttgt tataagttct 300
ggaagcaccg ttttcaggat caccaccatg cccgcggacg aatttccaga gataacgcct 360
gccgagtctg gaataacctt cgaagttgac acttcgctcc tcgaggaaat ggttgaaaag 420
gtcatcttcg ccgctgccaa agacgagttc atgcgaaatc tgaatggagt tttctgggaa 480
ctccacaaga atcttctcag gctggttgca agtgatggtt tcagacttgc acttgctgaa 540
gagcagatag aaaacgagga agaggcgagt ttcttgctct ctttgaagag catgaaagaa 600
gttcaaaacg tgctggacaa cacaacggag ccgactataa cggtgaggta cgatggaaga 660
agggtttctc tgcgcacaaa tgatgtagaa acggatgaga gagtggtcga cgctgaattt 720
cccgattaca aaagggtgat ccccgaaact ttcaaaacga aagtgggtgt ttccagaaaa 780
gaactcaggg aatctttgaa gaggtgatg gtgattgccg gcaaggggag cgagtccgtg 840
aagttcgaaa tagaagaaaa cgttatgaga cttgtgagca agagcccgga ttatggagaa 900
gtggtcgatg aagttgaagt tcaaaaagaa ggggaagatc tcgtgatcgc tttcaacccg 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaaat gaacttcgtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggatacct ttacatagtg 1080
atgcccatca gactggca 1098
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<210> 144

<211> 366

<212> PRT

<213> *Thermatoga maritima*

<400> 144

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Met Lys Val Thr Val Thr Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile
  1                      5                      10                      15

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly
    20                      25                      30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp
    35                      40                      45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly
    50                      55                      60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys
    65                      70                      75                      80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu
    85                      90                      95
```

Val Ile Ser Ser Gly Ser Thr Val Phe Arg Ile Thr Thr Met Pro Ala
100 105 110
Asp Glu Phe Pro Glu Ile Thr Pro Ala Glu Ser Gly Ile Thr Phe Glu
115 120 125
Val Asp Thr Ser Leu Leu Glu Glu Met Val Glu Lys Val Ile Phe Ala
130 135 140
Ala Ala Lys Asp Glu Phe Met Arg Asn Leu Asn Gly Val Phe Trp Glu
145 150 155 160
Leu His Lys Asn Leu Leu Arg Leu Val Ala Ser Asp Gly Phe Arg Leu
165 170 175
Ala Leu Ala Glu Glu Gln Ile Glu Asn Glu Glu Glu Ala Ser Phe Leu
180 185 190
Leu Ser Leu Lys Ser Met Lys Glu Val Gln Asn Val Leu Asp Asn Thr
195 200 205
Thr Glu Pro Thr Ile Thr Val Arg Tyr Asp Gly Arg Arg Val Ser Leu
210 215 220
Ser Thr Asn Asp Val Glu Thr Val Met Arg Val Val Asp Ala Glu Phe
225 230 235 240
Pro Asp Tyr Lys Arg Val Ile Pro Glu Thr Phe Lys Thr Lys Val Val
245 250 255
Val Ser Arg Lys Glu Leu Arg Glu Ser Leu Lys Arg Val Met Val Ile
260 265 270
Ala Ser Lys Gly Ser Glu Ser Val Lys Phe Glu Ile Glu Glu Asn Val
275 280 285
Met Arg Leu Val Ser Lys Ser Pro Asp Tyr Gly Glu Val Val Asp Glu
290 295 300
Val Glu Val Gln Lys Glu Gly Glu Asp Leu Val Ile Ala Phe Asn Pro
305 310 315 320
Lys Phe Ile Glu Asp Val Leu Lys His Ile Glu Thr Glu Glu Ile Glu
325 330 335
Met Asn Phe Val Asp Ser Thr Ser Pro Cys Gln Ile Asn Pro Leu Asp
340 345 350

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala
 355 360 365

<210> 145
 <211> 972
 <212> DNA
 <213> *Thermatoga maritima*

<400> 145
 atgccagtca cgttttctcac aggtactgca gaaactcaga aggaagaatt gataaagaaa 60
 ctccctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120
 gatttcataa ggtctttact caggacaaag acgatctttt ccaacaagac gatcattgac 180
 atcgtcaatt tcgatgagtg gaaagcacag gagcagaagc gtctcgttga acttttgaaa 240
 aacgtaccgg aagacgttca tatcttcatc cgttctcaaa aaacaggtgg aaagggagta 300
 gcgctggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtggat agaaaagcgc 360
 ttcagggaga atggtttgct catcgataaa gatgcccttc agctgttttt ctccaagggt 420
 ggaacgaacg acctgatcat agaaagggag attgaaaaac tgaaagctta ttccgaggac 480
 agaaagataa cggtagaaga cgtggaagag gtcgttttta cctatcagac tccgggatac 540
 gatgattttt gctttgctgt ttccgaagga aaaaggaagc tcgctcactc tcttctgtcg 600
 cagctgtgga aaaccacaga gtccgtggtg attgccactg tccttgcgaa tcacttcttg 660
 gatctcttca aaatcctcgt tcttgtagaca aagaaaagat actacacctg gcctgatgtg 720
 tccaggggtg ccaaagagct gggaattccc gttcctcgtg tggctcgttt cctcggtttc 780
 tcctttaaga cctggaaatt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840
 gttagaaga tactgaggga tctctacgat ctggacagag ccgtgaaaag cgaagaagat 900
 ccaaaaccgt tcttccacga gttcatagaa gaggtggcac tggatgtata ttctcttcag 960
 agagatgaag aa 972

<210> 146
 <211> 324
 <212> PRT
 <213> *Thermatoga maritima*

<400> 146
 Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu
 1 5 10 15
 Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile
 20 25 30
 His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg
 35 40 45
 Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe
 50 55 60

Asp	Glu	Trp	Lys	Ala	Gln	Glu	Gln	Lys	Arg	Leu	Val	Glu	Leu	Leu	Lys	65	70	75	80
Asn	Val	Pro	Glu	Asp	Val	His	Ile	Phe	Ile	Arg	Ser	Gln	Lys	Thr	Gly	85	90	95	
Gly	Lys	Gly	Val	Ala	Leu	Glu	Leu	Pro	Lys	Pro	Trp	Glu	Thr	Asp	Lys	100	105	110	
Trp	Leu	Glu	Trp	Ile	Glu	Lys	Arg	Phe	Arg	Glu	Asn	Gly	Leu	Leu	Ile	115	120	125	
Asp	Lys	Asp	Ala	Leu	Gln	Leu	Phe	Phe	Ser	Lys	Val	Gly	Thr	Asn	Asp	130	135	140	
Leu	Ile	Ile	Glu	Arg	Glu	Ile	Glu	Lys	Leu	Lys	Ala	Tyr	Ser	Glu	Asp	145	150	155	160
Arg	Lys	Ile	Thr	Val	Glu	Asp	Val	Glu	Glu	Val	Val	Phe	Thr	Tyr	Gln	165	170	175	
Thr	Pro	Gly	Tyr	Asp	Asp	Phe	Cys	Phe	Ala	Val	Ser	Glu	Gly	Lys	Arg	180	185	190	
Lys	Leu	Ala	His	Ser	Leu	Leu	Ser	Gln	Leu	Trp	Lys	Thr	Thr	Glu	Ser	195	200	205	
Val	Val	Ile	Ala	Thr	Val	Leu	Ala	Asn	His	Phe	Leu	Asp	Leu	Phe	Lys	210	215	220	
Ile	Leu	Val	Leu	Val	Thr	Lys	Lys	Arg	Tyr	Tyr	Thr	Trp	Pro	Asp	Val	225	230	235	240
Ser	Arg	Val	Ser	Lys	Glu	Leu	Gly	Ile	Pro	Val	Pro	Arg	Val	Ala	Arg	245	250	255	
Phe	Leu	Gly	Phe	Ser	Phe	Lys	Thr	Trp	Lys	Phe	Lys	Val	Met	Asn	His	260	265	270	
Leu	Leu	Tyr	Tyr	Asp	Val	Lys	Lys	Val	Arg	Lys	Ile	Leu	Arg	Asp	Leu	275	280	285	
Tyr	Asp	Leu	Asp	Arg	Ala	Val	Lys	Ser	Glu	Glu	Asp	Pro	Lys	Pro	Phe	290	295	300	
Phe	His	Glu	Phe	Ile	Glu	Glu	Val	Ala	Leu	Asp	Val	Tyr	Ser	Leu	Gln	305	310	315	320

Arg Asp Glu Glu

<210> 147

<211> 936

<212> DNA

<213> *Thermatoga maritima*

<400> 147

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atgaacgatt tgatcagaaa gtacgctaaa gatcaactgg aaactttgaa aaggatcata 60
gaaaagtctg aaggaatatc catcctcata aatggagaag atctctcgta tccgagagaa 120
gtatcccttg aacttcccga gtacgtggag aaatttcccc cgaaggcctc ggatgttctg 180
gagatagatc ccgaggggga gaacataggc atagacgaca tcagaacgat aaaggacttc 240
ctgaactaca gccccgagct ctacacgaga aagtacgtga tagtccacga ctgtgaaaga 300
atgacccagc aggcggcgaa cgcgtttctg aaggcccttg aagaaccacc agaatacgct 360
gtgatcgttc tgaacactcg ccgctggcat tatctactgc cgacgataaa gagccgagtg 420
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
gatctctggg aggaacttcc acttcttgag agagacttca aaacggctct cgaagcctac 540
aaacttggtg cggaaaaact ttctggattg atggaaagtc tcaaagtttt ggagacggaa 600
aaactcttga aaaaggtcct ttcaaaaggc ctcgaagggt atctcgcatg tagggagctc 660
ctggagagat tttcaaagggt ggaatcgaag gaattctttg cgctttttga tcagggtgact 720
aacacgataa caggaaaaga cgcgtttctt ttgatccaga gactgacaag aatcattctc 780
cacgaaaaca catgggaaag cgttgaagat caaaaaagcg tgtctttcct cgattcaatt 840
ctcaggggtg agatagcgaa tctgaacaac aaactcactc tgatgaacat cctcgcgata 900
cacagagaga gaaagagagg tgtcaacgct tggagc 936
```

<210> 148

<211> 311

<212> PRT

<213> *Thermatoga maritima*

<400> 148

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Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
  1             5             10             15

Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
          20             25             30

Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
          35             40             45

Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
          50             55             60

Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
          65             70             75             80
```

Leu Asn Tyr Ser Pro Glu Leu Tyr Thr Arg Lys Tyr Val Ile Val His
 85 90 95

Asp Cys Glu Arg Met Thr Gln Gln Ala Ala Asn Ala Phe Leu Lys Ala
 100 105 110

Leu Glu Glu Pro Pro Glu Tyr Ala Val Ile Val Leu Asn Thr Arg Arg
 115 120 125

Trp His Tyr Leu Leu Pro Thr Ile Lys Ser Arg Val Phe Arg Val Val
 130 135 140

Val Asn Val Pro Lys Glu Phe Arg Asp Leu Val Lys Glu Lys Ile Gly
 145 150 155 160

Asp Leu Trp Glu Glu Leu Pro Leu Leu Glu Arg Asp Phe Lys Thr Ala
 165 170 175

Leu Glu Ala Tyr Lys Leu Gly Ala Glu Lys Leu Ser Gly Leu Met Glu
 180 185 190

Ser Leu Lys Val Leu Glu Thr Glu Lys Leu Leu Lys Lys Val Leu Ser
 195 200 205

Lys Gly Leu Glu Gly Tyr Leu Ala Cys Arg Glu Leu Leu Glu Arg Phe
 210 215 220

Ser Lys Val Glu Ser Lys Glu Phe Phe Ala Leu Phe Asp Gln Val Thr
 225 230 235 240

Asn Thr Ile Thr Gly Lys Asp Ala Phe Leu Leu Ile Gln Arg Leu Thr
 245 250 255

Arg Ile Ile Leu His Glu Asn Thr Trp Glu Ser Val Glu Asp Lys Ser
 260 265 270

Val Ser Phe Leu Asp Ser Ile Leu Arg Val Lys Ile Ala Asn Leu Asn
 275 280 285

Asn Lys Leu Thr Leu Met Asn Ile Leu Ala Ile His Arg Glu Arg Lys
 290 295 300

Arg Gly Val Asn Ala Trp Ser
 305 310

<210> 149

<211> 423
 <212> DNA
 <213> *Thermatoga maritima*

<400> 149
 atgtctttct tcaacaagat cataactcata ggaagactcg tgagagatcc cgaagagaga 60
 tacacgctca gcggaactcc agtcaccacc ttcaccatag cgggtggacag gggtcccaga 120
 aagaacgcgc cggacgacgc tcaaacgact gatttcttca ggatcgtcac ctttggaaga 180
 ctggcagagt tcgctagaac ctatctcacc aaaggaaggc tcgttctcgt cgaaggtgaa 240
 atgagaatga gaagatggga aacacccact ggagaaaaga gggatatctcc ggaggttgtc 300
 gcaaacgttg ttagattcat ggacagaaaa cctgctgaaa cagttagcga gactgaagag 360
 gagctggaaa taccggaaga agacttttcc agcgatacct tcagtgaaga tgaaccacca 420
 ttt 423

<210> 150
 <211> 141
 <212> PRT
 <213> *Thermatoga maritima*

<400> 150
 Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp
 1 5 10 15
 Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Thr Phe Thr
 20 25 30
 Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln
 35 40 45
 Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe
 50 55 60
 Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu
 65 70 75 80
 Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser
 85 90 95
 Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala
 100 105 110
 Glu Thr Val Ser Glu Thr Glu Glu Glu Leu Glu Ile Pro Glu Glu Asp
 115 120 125
 Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe
 130 135 140

<210> 151
 <211> 1353
 <212> DNA
 <213> *Thermatoga maritima*

<400> 151
 atgcgtgttc ccccgacacaa cttagaggcc gaagttgctg tgctcggaag catattgata 60
 gatccgtcgg taataaacga cgttcttgaa attttgagcc acgaagattt ctatctgaaa 120
 aaacaccaac acatcttcag agcgatggaa gagctttacg acgaaggaaa accggtggac 180
 gtgggtttccg tctgtgacaa gcttcaaagc atgggaaaac tcgaggaagt aggtggagat 240
 ctggaagtgg ccagctcgc tgaggctgtg ccagttctg cacacgcact tcactacgcg 300
 gagatcgtca aggaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360
 gaaagtgcct acatggaaga agatgtggag atcctgctcg acaacgcaga aaagatgata 420
 ttcgagatct cagagatgaa aacgacaaaa tcctacgata atctgagagg catcatgcac 480
 cgggtgtttg aaaacctgga gaacttcagg gaaagagcca accttataga acccggtgtg 540
 ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac agggttccac 600
 agctccgatac tggtgataat agcagcgaga ccctccatgg gaaaaacctc cttcgcaactc 660
 tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatatt cagtctcgag 720
 atgtccaagg aacagctcgc tcaaagacta ctacagatgg agtccggtgt ggatctttac 780
 agcatcagaa caggatacct ggatcaggag aagtgggaaa gactcacaat agcggcttct 840
 aaactctaca aagcacccat agttgtggac gatgagtcac tcctcgatcc gcgatcgttg 900
 agggcaaaaag cgagaaggat gaaaaaagaa tacgatgtaa aagccatttt tgtcgactat 960
 ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagata 1020
 tcgagatctc tgaagctcct tgcgaggga ctcgacatag tggatgatac gctttcacag 1080
 ctttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtga cctcagggaa 1140
 tccggtgcga tagaacagga cgcagacaca gtcattctca tctacaggga ggaatattac 1200
 aggagcaaaa aatccaaaga ggaaagcaag cttcacgaac ctacgaagc tgaaatcata 1260
 ataggtaaac agagaaacgg tcccgttga acgatcaact tgatcttcga cccagaacg 1320
 gttacgttcc atgaagtcga tgtggtgcat tca 1353

<210> 152
 <211> 451
 <212> PRT
 <213> *Thermatoga maritima*

<400> 152
 Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly
 1 5 10 15
 Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu
 20 25 30
 Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala
 35 40 45
 Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val

50		55		60
Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Glu Val Gly Gly Asp				
65		70		75 80
Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala				
	85		90	95
Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu				
	100		105	110
Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp				
	115		120	125
Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser				
	130		135	140
Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His				
145		150		155 160
Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile				
	165		170	175
Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu				
	180		185	190
Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala				
	195		200	205
Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg				
	210		215	220
Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu				
225		230		235 240
Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly				
	245		250	255
Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp				
	260		265	270
Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val				
	275		280	285
Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala				
	290		295	300
Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr				

305	310	315	320
Leu Gln Leu Met His Leu Lys Gly Arg Lys Glu Ser Arg Gln Gln Glu			
325	330	335	
Ile Ser Glu Ile Ser Arg Ser Leu Lys Leu Leu Ala Arg Glu Leu Asp			
340	345	350	
Ile Val Val Ile Ala Leu Ser Gln Leu Ser Arg Ala Val Glu Gln Arg			
355	360	365	
Glu Asp Lys Arg Pro Arg Leu Ser Asp Leu Arg Glu Ser Gly Ala Ile			
370	375	380	
Glu Gln Asp Ala Asp Thr Val Ile Phe Ile Tyr Arg Glu Glu Tyr Tyr			
385	390	395	400
Arg Ser Lys Lys Ser Lys Glu Glu Ser Lys Leu His Glu Pro His Glu			
405	410	415	
Ala Glu Ile Ile Ile Gly Lys Gln Arg Asn Gly Pro Val Gly Thr Ile			
420	425	430	
Thr Leu Ile Phe Asp Pro Arg Thr Val Thr Phe His Glu Val Asp Val			
435	440	445	
Val His Ser			
450			

<210> 153
 <211> 1695
 <212> DNA
 <213> *Thermatoga maritima*

<400> 153
 gtgattcctc gagaggtcat cgaggaaata aaagaaaagg ttgacatcgt agaggtcatt 60
 tccgagtacg tgaatcttac ccgggtaggt tctcctaca gggctctctg tccctttcat 120
 tcagaaacca atccttcttt ctacgttcat ccgggtttga agatatacca ttgtttcggc 180
 tgcggtgcga gtggagacgt catcaaattt cttcaagaaa tggaagggat cagtttccag 240
 gaagcgctgg aaagacttgc caaaagagct gggattgatc tttctctcta cagaacagaa 300
 gggacttctg aatacggaaa atacattcgt ttgtacgaag aaacgtggaa aaggtacgtc 360
 aaagagctgg agaaatcgaa agaggcaaaa gactatttaa aaagcagagg cttctctgaa 420
 gaagatatag caaagtctcg ctttgggtac gtccccaaga gatccagcat ctctatagaa 480
 gttgcagaag gcatgaacat aacactggaa gaacttgtca gatacgggat cgcgctgaaa 540
 aagggtgatc gattcgttga tagattcgaa ggaagaatcg ttgttccaat aaagaacgac 600
 agtggtcata ttgtggcttt tgggtggcgt gctctcggca acgaagaacc gaagtatttg 660
 aactctccag agaccagga tttttcgaag aagaagaccc tttttctctt cgatgaggcg 720

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aaaaaagtgg caaaagaggt tggttttttc gtcacccaccg aaggctactt cgacgcgctc 780
gcattcagaa aggatggaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840
gaggcgattc taaaactttc ggcgtattcg aaaaacgtca tactgtgttt cgataatgac 900
aaagcaggct tcagagccac tctcaaatcc ctcgaggatc tcctagacta cgaattcaac 960
gtgcttgtgg caacccccctc tccttacaaa gaccagatg aactctttca gaaagaagga 1020
gaaggttcat tgaaaaagat gctgaaaaac tcgcgttcgt tcgaatattt tctggtgacg 1080
gctggtgagg tcttctttga caggaacagc cccgcgggtg tgagatccta cttttctttc 1140
ctcaaagggt ggggtccaaaa gatgagaagg aaaggatatt tgaaacacat agaaaatctc 1200
gtgaatgagg tttcatcttc tctccagata ccagaaaacc agattttgaa cttttttgaa 1260
agcgacaggt ctaacactat gcctgttcat gagaccaagt cgtcaaagggt ttacgatgag 1320
gggagaggac tggcttattt gtttttgaac tacgaggatt tgagggaaaa gattctggaa 1380
ctggacttag aggtactgga agataaaaac gcgagggagt ttttcaagag agtctcactg 1440
ggagaagatt tgaacaaaagt catagaaaac ttcccaaaag agctgaaaga ctggattttt 1500
gagacaatag aaagcattcc tcctccaaag gatcccgaga aattcctcgg tgacctctcc 1560
gaaaagttga aaatccgacg gatagagaga cgtatcgag aaatagatga tatgataaag 1620
aaagcttcaa acgatgaaga aaggcgtctt cttctctcta tgaaagtgga tctcctcaga 1680
aaaataaaga ggagg                                     1695

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<210> 154
 <211> 565
 <212> PRT
 <213> *Thermatoga maritima*

<400> 154
 Met Ile Pro Arg Glu Val Ile Glu Glu Ile Lys Glu Lys Val Asp Ile
 1 5 10 15

 Val Glu Val Ile Ser Glu Tyr Val Asn Leu Thr Arg Val Gly Ser Ser
 20 25 30

 Tyr Arg Ala Leu Cys Pro Phe His Ser Glu Thr Asn Pro Ser Phe Tyr
 35 40 45

 Val His Pro Gly Leu Lys Ile Tyr His Cys Phe Gly Cys Gly Ala Ser
 50 55 60

 Gly Asp Val Ile Lys Phe Leu Gln Glu Met Glu Gly Ile Ser Phe Gln
 65 70 75 80

 Glu Ala Leu Glu Arg Leu Ala Lys Arg Ala Gly Ile Asp Leu Ser Leu
 85 90 95

 Tyr Arg Thr Glu Gly Thr Ser Glu Tyr Gly Lys Tyr Ile Arg Leu Tyr
 100 105 110

 Glu Glu Thr Trp Lys Arg Tyr Val Lys Glu Leu Glu Lys Ser Lys Glu
 115 120 125

Ala Lys Asp Tyr Leu Lys Ser Arg Gly Phe Ser Glu Glu Asp Ile Ala
130 135 140
Lys Phe Gly Phe Gly Tyr Val Pro Lys Arg Ser Ser Ile Ser Ile Glu
145 150 155 160
Val Ala Glu Gly Met Asn Ile Thr Leu Glu Glu Leu Val Arg Tyr Gly
165 170 175
Ile Ala Leu Lys Lys Gly Asp Arg Phe Val Asp Arg Phe Glu Gly Arg
180 185 190
Ile Val Val Pro Ile Lys Asn Asp Ser Gly His Ile Val Ala Phe Gly
195 200 205
Gly Arg Ala Leu Gly Asn Glu Glu Pro Lys Tyr Leu Asn Ser Pro Glu
210 215 220
Thr Arg Tyr Phe Ser Lys Lys Lys Thr Leu Phe Leu Phe Asp Glu Ala
225 230 235 240
Lys Lys Val Ala Lys Glu Val Gly Phe Phe Val Ile Thr Glu Gly Tyr
245 250 255
Phe Asp Ala Leu Ala Phe Arg Lys Asp Gly Ile Pro Thr Ala Val Ala
260 265 270
Val Leu Gly Ala Ser Leu Ser Arg Glu Ala Ile Leu Lys Leu Ser Ala
275 280 285
Tyr Ser Lys Asn Val Ile Leu Cys Phe Asp Asn Asp Lys Ala Gly Phe
290 295 300
Arg Ala Thr Leu Lys Ser Leu Glu Asp Leu Leu Asp Tyr Glu Phe Asn
305 310 315 320
Val Leu Val Ala Thr Pro Ser Pro Tyr Lys Asp Pro Asp Glu Leu Phe
325 330 335
Gln Lys Glu Gly Glu Gly Ser Leu Lys Lys Met Leu Lys Asn Ser Arg
340 345 350
Ser Phe Glu Tyr Phe Leu Val Thr Ala Gly Glu Val Phe Phe Asp Arg
355 360 365
Asn Ser Pro Ala Gly Val Arg Ser Tyr Leu Ser Phe Leu Lys Gly Trp
370 375 380

Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu
 385 390 395 400

Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu
 405 410 415

Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr
 420 425 430

Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe
 435 440 445

Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu
 450 455 460

Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu
 465 470 475 480

Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys
 485 490 495

Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro
 500 505 510

Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile
 515 520 525

Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn
 530 535 540

Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg
 545 550 555 560

Lys Ile Lys Arg Arg
 565

<210> 155

<211> 804

<212> DNA

<213> *Thermus thermophilus*

<400> 155

atggctctac acccggtctca ccctggggca ataatcgggc acgaggccgt tctcgccctc 60
 cttccccgcc tcaccgccc gacctgctc ttctccggcc ccgagggggg ggggcggcgc 120
 accgtggccc gctggtacgc ctgggggctc aaccgcgget tccccccgcc ctccctgggg 180
 gagcaccggg acgtcctcga ggtggggccc aaggcccggg acctccgggg ccgggcccag 240

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gtgcggtggtg aggaggtggc gcccctcttg gagtgggtgct ccagccaccc ccgggagcgg 300
gtgaaggtgg ccactctgga ctcggccac ctctcaccg aggcgcgcgc caacgccctc 360
ctcaagctcc tggaggagcc ccttctctac gcccgcatcg tctcatcgcc cccaagccgc 420
gccaccctcc tccccaccct ggccctcccg gccacggagg tggcattcgc ccccgtgccc 480
gaggaggccc tgcgcgccct caccacaggac ccggagctcc tccgctacgc cgcggggggc 540
ccgggcccgc tccttagggc cctccaggac ccggaggggt accgggcccgc catggccagg 600
gcgcaaaggg tcctgaaagc cccgcccctg gagcgctcg ctttgcttcg ggagcttttg 660
gccgaggagg aggggggtcca cgccctccac gccgtcctaa agcgcccgga gcacctcctt 720
gccctggagc gggcgcgggga ggccctggag gggtagctga gccccgagct ggctcctcgcc 780
cggctggcct tagacttaga gaca
804

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<210> 156
<211> 268
<212> PRT
<213> Thermus thermophilus

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<400> 156
Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala
  1             5             10             15

Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser
      20             25             30

Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp
      35             40             45

Gly Leu Asn Arg Gly Phe Pro Pro Pro Ser Leu Gly Glu His Pro Asp
      50             55             60

Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu
      65             70             75             80

Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His
      85             90             95

Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu
      100            105            110

Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro
      115            120            125

Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu
      130            135            140

Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro
      145            150            155            160

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Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr
 165 170 175
 Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu
 180 185 190
 Gly Tyr Arg Ala Arg Met Ala Arg Ala Gln Arg Val Leu Lys Ala Pro
 195 200 205
 Pro Leu Glu Arg Leu Ala Leu Leu Arg Glu Leu Leu Ala Glu Glu Glu
 210 215 220
 Gly Val His Ala Leu His Ala Val Leu Lys Arg Pro Glu His Leu Leu
 225 230 235 240
 Ala Leu Glu Arg Ala Arg Glu Ala Leu Glu Gly Tyr Val Ser Pro Glu
 245 250 255
 Leu Val Leu Ala Arg Leu Ala Leu Asp Leu Glu Thr
 260 265

<210> 157
 <211> 729
 <212> DNA
 <213> *Thermus thermophilus*

<400> 157
 atgctggacc tgagggaggt gggggaggcg gagtggaagg ccctaaagcc ccttttggaa 60
 agcgtgcccg agggcgctccc cgtcctcctc ctggacccta agccaagccc ctcccgggcg 120
 gccttctacc ggaaccggga aaggcgggac ttccccaccc ccaaggggaa ggacctggtg 180
 cggcacctgg aaaaccgggc caagcgccctg gggctcaggc tcccgggcg ggtggcccag 240
 tacctggcct ccctggaggg ggacctcgag gccctggagc gggagctgga gaagcttgcc 300
 ctctctctccc caccctcac cctggagaag gtggagaagg tgggtggcct gagggccccc 360
 ctacacgggct ttgacctggt gcgctccgct ctggagaagg accccaagga ggccctcctg 420
 cgcctaggcg gcctcaagga ggagggggag gagccctca ggctcctcg ggccctctcc 480
 tggcagttcg ccctcctcgc ccgggccttc ttctcctcc gggaaaaccc caggcccaag 540
 gaggaggacc tcgcccgcct cgaggcccac ccctacgccg cccgccgcgc cctggaggcg 600
 gcgaagcgcc tcacggaaga ggccctcaag gaggccttg acgccctcat ggaggcggaa 660
 aagagggcca agggggggaa agaccctggt ctgcctctgg aggcggcggt cctccgcctc 720
 gcccgttga 729

<210> 158
 <211> 292
 <212> PRT
 <213> *Thermus thermophilus*

<400> 158

Met Val Ile Ala Phe Thr Gly Asp Pro Phe Leu Ala Arg Glu Ala Leu
1 5 10 15

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr
20 25 30

Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly
35 40 45

Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala
50 55 60

Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu
65 70 75 80

Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg
85 90 95

Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His
100 105 110

Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val
115 120 125

Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg
130 135 140

Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys
145 150 155 160

Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu
165 170 175

Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu
180 185 190

Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala
195 200 205

Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg
210 215 220

Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His
225 230 235 240

Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu
245 250 255

Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg
260 265 270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu
275 280 285

Arg Leu Ala Arg
290

<210> 159
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 159
gtgtgtcata tgagtaagga ttctgtccac cttcacc 37

<210> 160
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
gtgtgtggat ccgggggacta ctcggaagta aggg 34

<210> 161
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gtgtgtcata tggaaaccac aatattccag ttccag 36

<210> 162

<211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 162
 gtgtgtggat cttatccac catgagaagt atttttcac 39

 <210> 163
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 163
 gtgtgtcata tggaaaaagt tttttttgga aaaaactcca g 41

 <210> 164
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 164
 gtgtgtggat ccttaatccg cctgaacggc taacg 35

 <210> 165
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 165
 gtgtgtcata tgaactacgt tcccttcgag agaaagtaca g 41

 <210> 166

<211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 166
 gtgtgtggat ccttaaaaca gcctcgtccc gctgga 36

 <210> 167
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 167
 gtgtgtcata tgcgcgtaa ggtggacagg gag 33

 <210> 168
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 168
 tgtgtctcga gtcattggcta caccctcatc ggcatt 35

 <210> 169
 <211> 47
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 169
 gtgtgtcata tgctcaataa ggtttttata ataggaagac ttacggg 47

 <210> 170

<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 170
gtgtggatcc ttaaaaaggt atttcgtcct cttcatcgg

39

<210> 171
<211> 807
<212> DNA
<213> *Thermus thermophilus*

<400> 171
atggctcgag gcctgaaccg cgttttcttc atcggcgccc tcgccaccgc gccggacatg 60
cgctacacccc cggcgggggt cgccattttg gacctgaccc tcgccggtca ggacctgctt 120
ctttccgata acggggggga accggaggtg tcctggtacc accgggtgag gctcttaggc 180
cgccaggcgg agatgtgggg cgacctcttg gaccaagggc agctcgtctt cgtggagggc 240
cgcctggagt accgccagt ggaaagggag ggggagaagc ggagcgagct ccagatccgg 300
gccgacttcc ggaccccctg gacgaccggg ggaagaagcg ggcggaggac agccggggcc 360
agcccaggct ccgcgccgcc ctgaaccagg tcttctctcat gggcaacctg acccggggacc 420
cggaactccg ctacaccccc cagggcaccc cgggtggccc gctgggcctg gcggtgaacg 480
agcgccgcca gggggcgagg gagcgacccc acttcgtgga ggttcaggcc tggcgcgacc 540
tggcggagtg ggccgccgag ctgaggaagg gcgacggcct tttcgtgatc ggcaggttgg 600
tgaacgactc ctggaccagc tcacgcggcg agcggcgctt ccagaccggt gtggaggccc 660
tcaggctgga gcgccccacc cgtggacctg cccaggcctg cccaggccgg cggaacaggt 720
cccgcgaagt ccagacgggt ggggtggaca ttgacgaagg cttggaagac tttccgccgg 780
aggaggattt gccgttttga gcacgaa 807

<210> 172
<211> 266
<212> PRT
<213> *Thermus thermophilus*

<400> 172
Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr
1 5 10 15
Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu
20 25 30
Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro
35 40 45

Glu Val Ser Trp Tyr His Arg Val Arg Leu Leu Gly Arg Gln Ala Glu
 50 55 60
 Met Trp Gly Asp Leu Leu Asp Gln Gly Gln Leu Val Phe Val Glu Gly
 65 70 75 80
 Arg Leu Glu Tyr Arg Gln Trp Glu Arg Glu Gly Glu Lys Arg Ser Glu
 85 90 95
 Leu Gln Ile Arg Ala Asp Phe Leu Asp Pro Leu Asp Asp Arg Gly Lys
 100 105 110
 Lys Arg Ala Glu Asp Ser Arg Gly Gln Pro Arg Leu Arg Ala Ala Leu
 115 120 125
 Asn Gln Val Phe Leu Met Gly Asn Leu Thr Arg Asp Pro Glu Leu Arg
 130 135 140
 Tyr Thr Pro Gln Gly Thr Ala Val Ala Arg Leu Gly Leu Ala Val Asn
 145 150 155 160
 Glu Arg Arg Gln Gly Ala Glu Glu Arg Thr His Phe Val Glu Val Gln
 165 170 175
 Ala Trp Arg Asp Leu Ala Glu Trp Ala Ala Glu Leu Arg Lys Gly Asp
 180 185 190
 Gly Leu Phe Val Ile Gly Arg Leu Val Asn Asp Ser Trp Thr Ser Ser
 195 200 205
 Ser Gly Glu Arg Arg Phe Gln Thr Arg Val Glu Ala Leu Arg Leu Glu
 210 215 220
 Arg Pro Thr Arg Gly Pro Ala Gln Ala Cys Pro Gly Arg Arg Asn Arg
 225 230 235 240
 Ser Arg Glu Val Gln Thr Gly Gly Val Asp Ile Asp Glu Gly Leu Glu
 245 250 255
 Asp Phe Pro Pro Glu Glu Asp Leu Pro Phe
 260 265

<210> 173

<211> 992

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 173

```
aattccgaca tttcaattga atcgtttatt ccgcttgaaa aagaaggcaa gttgctcggt 60
gatgtgaaaa gaccggggag catcgctactg caggcgcgct ttttctctga aatcgtgaaa 120
aaactgccgc aacaaacggt ggaaatcgaa acggaagaca actttttgac gatcatccgc 180
tcggggcact cagaattccg cctcaatggg ctaaacgccg acgaatatcc gcgcctgccg 240
caaattgaag aagaaaacgt gtttcaaata ccggctgatt tattgaaaac cgtgattcgg 300
caaacggtgt tcgccgtttc tacatcggaa acgcgcccaa tcttgacagg tgtcaactgg 360
aaagttgaac atggcgagct tgtctgcaca gcgaccgaca gtcacatcgtt agccatgcgc 420
aaagtgaaaa ttgagtcgga aaatgaagta tcatacaacg tcgtcatccc tggaaaaaagt 480
cttaatgagc tcagcaaaat tttggatgac ggcaaccacc cgggtggacat cgtcatgaca 540
gccaatcaag tgctatttaa ggccgagcac cttctcttct tttcccggtc gcttgacggc 600
aactatccgg agacggcccg cttgattcca acagaaagca aaacgaccat gatcgtcaat 660
gcaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaac 720
aacgttgtga aactgacgac gcttcctgga ggaatgctcg aaatttcttc gatttctccg 780
agatcgggaa agtgacggag cagctgcaaa cggagtctct tgaaggggaa gagttgaaca 840
tttcgttcag cgcgaaatat atgatggacg cgttgcgggc gcttgatgga acagacattt 900
caaatcagct tcaactggggc catgcggccg ttctgttgc gcccgcttca accgattcga 960
tgcttcagct cattttgccg gtgagaacat at 992
```

<210> 174

<211> 334

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 174

```
Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
  1             5             10             15

Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
      20             25             30

Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
      35             40             45

Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
      50             55             60

Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
      65             70             75             80

Pro Gln Ile Glu Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
      85             90             95

Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
      100            105            110

Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu
```

115	120	125
Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys		
130	135	140
Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly		
145	150	155 160
Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His		
165	170	175
Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu		
180	185	190
His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr		
195	200	205
Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala		
210	215	220
Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu		
225	230	235 240
Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu		
245	250	255
Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu		
260	265	270
Gln Thr Glu Ser Leu Glu Gly Glu Glu Leu Asn Ile Ser Phe Ser Ala		
275	280	285
Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln		
290	295	300
Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His		
305	310	315 320
Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr		
325	330	

<210> 175
 <211> 492
 <212> DNA
 <213> Bacillus stearothermophilus

 <400> 175

```

atgattaacc gcgtcatttt ggtcggcagg ttaacgagag atccggagtt gcgttacact 60
ccaagcggag tggctgttgc cacgtttacg ctgcggtca accgtccgtt taaaaatcag 120
cagggcgagc gggaaacgga ttttattcaa tgtgtcgttt ggcgccgcca ggcggaaaac 180
gtcgccaact ttttgaaaaa ggggagcttg gctggtgtcg atggccgact gcaaaccgc 240
agctatgaaa atcaagaagg tcggcgtgtg tacgtgacgg aagtgggtggc tgatagcgtc 300
caatttcttg agccgaaagg aacgagcgag cagcgagggg cgacagcagg cggctactat 360
ggggatccat tcccattcgg gcaagatcag aaccaccaat atccgaacga aaaagggttt 420
ggccgcatcg atgacgatcc tttcgccaat gacggccagc cgatcgatat ttctgatgat 480
gatttgccgt tt 492

```

<210> 176

<211> 164

<212> PRT

<213> Bacillus stearothermophilus

<400> 176

```

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
  1             5             10             15

```

```

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
             20             25             30

```

```

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
             35             40             45

```

```

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
             50             55             60

```

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Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
             65             70             75             80

```

```

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
             85             90             95

```

```

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
             100             105             110

```

```

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
             115             120             125

```

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Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp
             130             135             140

```

```

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
             145             150             155             160

```

Asp Leu Pro Phe

<210> 177
 <211> 1044
 <212> DNA
 <213> Bacillus stearothermophilus

<400> 177
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 tacggcaatg agccgttttt attaacggaa acgtatgagc gattggtgaa cgcagcgctt 120
 ggccccgagg agcgggagtg gaacttggct gtgtacgact gcgaggaaac gccgatcgag 180
 gcggcgcttg aggaggccga gacggtgccg tttttcggcg agcggcggtgt cattctcatc 240
 aagcatccat attttttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300
 ctggaggcgt acttgaaggc gccgtcgccg ttttcgatcg tcgtcttttt cgcgccgtac 360
 gagaagcttg atgagcgaaa aaaaattacg aagctcgcca aagagcaaag cgaagtcgtc 420
 atcgccgccc cgctcgccga agcggagctg cgtgcctggg tgcggcgccg catcgagagc 480
 caaggggccc aagcaagcga cgaggcgatt gatgtcctgt tgcggcgggc cgggacgcag 540
 ctttccgcct tggcgaatga aatcgataaa ttggccctgt ttgccggatc gggcggaacc 600
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 cttgtcgagc aagtggcgaa gcgcgacatt ccagcagcgt tgcagacgtt ttatgatctg 720
 cttgaaaaca atgaagagcc gatcaaaatt ttggcgcttg tcgccgcca tttccgcttg 780
 ctttcgcaag tgaaatggct tgctcctta ggctacggac aggcgcaaat tgctgcggcg 840
 ctcaaggtgc acccggttccg cgtcaagctc gctcttgctc aagcggcccg cttcgctgac 900
 ggagagcttg ctgaggcgat caacgagctc gctgacgccg attacgaagt gaaaagcggg 960
 gcggtcgatc gccggttggc cgttgagctg cttctgatgc gctggggcgc ccgcccggcg 1020
 caagcggggc gccacggccg gcgg 1044

<210> 178
 <211> 348
 <212> PRT
 <213> Bacillus stearothermophilus

<400> 178
 Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro
 1 5 10 15
 Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr
 20 25 30
 Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn
 35 40 45
 Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu
 50 55 60
 Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile

65		70		75		80
Lys His Pro Tyr Phe Phe Thr Ser Glu Lys Glu Lys Glu Ile Glu His						
	85			90		95
Asp Leu Ala Lys Leu Glu Ala Tyr Leu Lys Ala Pro Ser Pro Phe Ser						
	100			105		110
Ile Val Val Phe Phe Ala Pro Tyr Glu Lys Leu Asp Glu Arg Lys Lys						
	115			120		125
Ile Thr Lys Leu Ala Lys Glu Gln Ser Glu Val Val Ile Ala Ala Pro						
	130			135		140
Leu Ala Glu Ala Glu Leu Arg Ala Trp Val Arg Arg Arg Ile Glu Ser						
145		150		155		160
Gln Gly Ala Gln Ala Ser Asp Glu Ala Ile Asp Val Leu Leu Arg Arg						
	165			170		175
Ala Gly Thr Gln Leu Ser Ala Leu Ala Asn Glu Ile Asp Lys Leu Ala						
	180			185		190
Leu Phe Ala Gly Ser Gly Gly Thr Ile Glu Ala Ala Ala Val Glu Arg						
	195			200		205
Leu Val Ala Arg Thr Pro Glu Glu Asn Val Phe Val Leu Val Glu Gln						
	210			215		220
Val Ala Lys Arg Asp Ile Pro Ala Ala Leu Gln Thr Phe Tyr Asp Leu						
225		230		235		240
Leu Glu Asn Asn Glu Glu Pro Ile Lys Ile Leu Ala Leu Leu Ala Ala						
	245			250		255
His Phe Arg Leu Leu Ser Gln Val Lys Trp Leu Ala Ser Leu Gly Tyr						
	260			265		270
Gly Gln Ala Gln Ile Ala Ala Ala Leu Lys Val His Pro Phe Arg Val						
	275			280		285
Lys Leu Ala Leu Ala Gln Ala Ala Arg Phe Ala Asp Gly Glu Leu Ala						
	290			295		300
Glu Ala Ile Asn Glu Leu Ala Asp Ala Asp Tyr Glu Val Lys Ser Gly						
305		310		315		320
Ala Val Asp Arg Arg Leu Ala Val Glu Leu Leu Leu Met Arg Trp Gly						

325

330

335

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg
 340 345

<210> 179

<211> 757

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 179

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aaagcggcca gtttgttgtt ggcgaaacgt ttgttttgtc tgtccccaat cggagtttcc 180
ccgtgtctag agtgccgcaa ctgccggcgc atcgactccg gcaaccaccc tgacgtccgg 240
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gtggcggtat tgctgactga gcaataccac cgcttgctag ggacgatcgt ttcccgcgtg 480
caagtgcctt cgttcgcggc gttgccgcgc gcagagctcg cccagggact tgtcgaggag 540
cacgtgccgt tgccgttggc gctgttggct gccatttga caaacagctt cgaggaagca 600
ctggcgcttg ccaaagatag ttggtttgcc gaggcgcgaa cattagtgt acaatggtat 660
gagatgctgg gcaagccgga gctgcagctt ttgtttttca tccacgaccg cttgtttccg 720
catttttttg aaagccatca gcttgacctt ggacttg 757

```

<210> 180

<211> 252

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 180

```

Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
  1             5             10             15

Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
      20             25             30

Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Leu Ala
      35             40             45

Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
      50             55             60

Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
      65             70             75             80

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Val Ile Gly Pro Asp Gly Gly Ser Ile Lys Lys Glu Gln Ile Glu Trp
85 90 95

Leu Gln Gln Glu Phe Ser Lys Thr Ala Val Glu Ser Asp Lys Lys Met
100 105 110

Tyr Ile Val Glu His Ala Asp Gln Met Thr Thr Ser Ala Ala Asn Ser
115 120 125

Leu Leu Lys Phe Leu Glu Glu Pro His Pro Gly Thr Val Ala Val Leu
130 135 140

Leu Thr Glu Gln Tyr His Arg Leu Leu Gly Thr Ile Val Ser Arg Cys
145 150 155 160

Gln Val Leu Ser Phe Arg Pro Leu Pro Pro Ala Glu Leu Ala Gln Gly
165 170 175

Leu Val Glu Glu His Val Pro Leu Pro Leu Ala Leu Leu Ala Ala His
180 185 190

Leu Thr Asn Ser Phe Glu Glu Ala Leu Ala Leu Ala Lys Asp Ser Trp
195 200 205

Phe Ala Glu Ala Arg Thr Leu Val Leu Gln Trp Tyr Glu Met Leu Gly
210 215 220

Lys Pro Glu Leu Gln Leu Leu Phe Phe Ile His Asp Arg Leu Phe Pro
225 230 235 240

His Phe Leu Glu Ser His Gln Leu Asp Leu Gly Leu
245 250

<210> 181

<211> 1677

<212> DNA

<213> Bacillus stearothermophilus

<400> 181

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tacttatttt ccggcccgcg cggtacagga aaaacgagcg cagcgaaaat ttctgccaaag 180
gcggtcaact gtgaacaggc gccagcggcg gagccatgca atgagtgtcc agcttgcttc 240
ggcattacga atggaacggg tcccgatgtg ctggaaattg acgctgcttc caacaaccgc 300
gtcgatgaaa ttcgtgatat ccgtgagaag gtgaaatttg cgccaacgtc ggcccgtac 360
aaagtgtata tcatcgacga ggtgcatatg ctgtcgatcg gtgcgtttta cgcgctgttg 420
aaaacgttgg aggagccgcc gaaacacgtc attttcattt tggccacgac cgagccgcac 480

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aaaattccgg cgacgatcat ttcccgtctg caacgggttcg attttcgccg catcccgttt 540
caggcgatcg ttccacggct aaagtacgtc gcaagcgccc aaggtgtcga ggcgtcagat 600
gaggcattgt ccgccatcgc ccgtgctgca gacgggggga tgcgcgatgc gctcagcttg 660
cttgatcaag ccatttcgtt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720
accggggctg catcatttgc cgccttatcg agcttcacgc aagccatcca ccgcaaagat 780
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gtggaggagg cgattcaaatt tgctgtcgtt gacgaagcgt tcacttcact gtcggaaatg 960
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aagtggacaa accacccgcg ccttctgttg gaagtggcgc ttgtgaaact ttgccatcca 1080
tcagccgcgc ccccgctcgt gtcggcttcc gagttggaac cgttgataaa gcggattgaa 1140
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gcgcgggtga aaaaactgtc caaaccgatg aaaacggggg gatataaagc cccggttggc 1260
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ccgttaatcg ccgaagcgaa gcggctgttt ggcgaagagc tgatcgaaat taaagaa 1677

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<210> 182

<211> 559

<212> PRT

<213> Bacillus stearothermophilus

<400> 182

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Val Ala Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Ala
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Asp Met Val Gly Gln Glu His Val Thr Lys Thr Leu Gln Ser Ala Leu
      20             25            30

Leu Gln His Lys Ile Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
      35             40            45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
      50             55            60

Glu Gln Ala Pro Ala Ala Glu Pro Cys Asn Glu Cys Pro Ala Cys Leu
      65             70            75            80

Gly Ile Thr Asn Gly Thr Val Pro Asp Val Leu Glu Ile Asp Ala Ala
      85             90            95

Ser Asn Asn Arg Val Asp Glu Ile Arg Asp Ile Arg Glu Lys Val Lys
      100            105            110

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Phe	Ala	Pro	Thr	Ser	Ala	Arg	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val	115	120	125	
His	Met	Leu	Ser	Ile	Gly	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	130	135	140	
Glu	Pro	Pro	Lys	His	Val	Ile	Phe	Ile	Leu	Ala	Thr	Thr	Glu	Pro	His	145	150	155	160
Lys	Ile	Pro	Ala	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Arg	Phe	Asp	Phe	Arg	165	170	175	
Arg	Ile	Pro	Leu	Gln	Ala	Ile	Val	Ser	Arg	Leu	Lys	Tyr	Val	Ala	Ser	180	185	190	
Ala	Gln	Gly	Val	Glu	Ala	Ser	Asp	Glu	Ala	Leu	Ser	Ala	Ile	Ala	Arg	195	200	205	
Ala	Ala	Asp	Gly	Gly	Met	Arg	Asp	Ala	Leu	Ser	Leu	Leu	Asp	Gln	Ala	210	215	220	
Ile	Ser	Phe	Ser	Asp	Gly	Lys	Leu	Arg	Leu	Asp	Asp	Val	Leu	Ala	Met	225	230	235	240
Thr	Gly	Ala	Ala	Ser	Phe	Ala	Ala	Leu	Ser	Ser	Phe	Ile	Glu	Ala	Ile	245	250	255	
His	Arg	Lys	Asp	Thr	Ala	Ala	Val	Leu	Gln	His	Leu	Glu	Thr	Met	Met	260	265	270	
Ala	Gln	Gly	Lys	Asp	Pro	His	Arg	Leu	Val	Glu	Asp	Leu	Ile	Leu	Tyr	275	280	285	
Tyr	Arg	Asp	Leu	Leu	Leu	Tyr	Lys	Thr	Ala	Pro	Tyr	Val	Glu	Gly	Ala	290	295	300	
Ile	Gln	Ile	Ala	Val	Val	Asp	Glu	Ala	Phe	Thr	Ser	Leu	Ser	Glu	Met	305	310	315	320
Ile	Pro	Val	Ser	Asn	Leu	Tyr	Glu	Ala	Ile	Glu	Leu	Leu	Asn	Lys	Ser	325	330	335	
Gln	Gln	Glu	Met	Lys	Trp	Thr	Asn	His	Pro	Arg	Leu	Leu	Leu	Glu	Val	340	345	350	
Ala	Leu	Val	Lys	Leu	Cys	His	Pro	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Ser	355	360	365	

Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala
 370 375 380

Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala
 385 390 395 400

Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys
 405 410 415

Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu
 420 425 430

Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu
 435 440 445

Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu
 450 455 460

Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu
 465 470 475 480

Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn
 485 490 495

Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val
 500 505 510

Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg
 515 520 525

Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala
 530 535 540

Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu
 545 550 555

<210> 183

<211> 4301

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 183

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 gaggagaaaa gctggcattt ttattttcag ttcgacaacg tgctgccggt tcatgtatac 180
 aaaacgtttg ccgatcggct gcagacggcg ttccgccata tcgccgcgct ccgccatacg 240

atggaggtcg	aagcgccgcg	cgtaactgag	gcggatgtgc	aggcgtattg	gccgctttgc	300
cttgccgagc	tgcaagaagg	catgtcgccg	cttgtcgatt	ggctcagccg	gcagacgcct	360
gagctgaaag	gaaacaagct	gcttgtcggt	gcccgccatg	aagcggaagc	gctggcgatc	420
aaacggcggg	tcgccaaaaa	aatcgctgat	gtgtacgctt	cgtttggtt	tccccccctt	480
cagcttgacg	tcagcgtcga	gccgtccaag	caagaaatgg	aacagttttt	ggcgcaaaaa	540
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gatacgttcg	tccgtgattt	ggtcatcatc	gccaacgatt	tgaacgaaat	cgccgcaaac	960
gaacggcaag	atacggcgcc	ggaaggggaa	aagagggtcg	agctccattt	gcataccccg	1020
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```

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```

<210> 184

<211> 1433

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 184

```

Met Val Thr Lys Glu Gln Lys Glu Arg Phe Leu Ile Leu Leu Glu Gln
  1              5              10              15

```

```

Leu Lys Met Thr Ser Asp Glu Trp Met Pro His Phe Arg Glu Ala Ala
      20              25              30

```

```

Ile Arg Lys Val Val Ile Asp Lys Glu Glu Lys Ser Trp His Phe Tyr
      35              40              45

```

```

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala
      50              55              60

```

```

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr
      65              70              75              80

```

```

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr
      85              90              95

```

```

Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val
      100             105             110

```

Asp	Trp	Leu	Ser	Arg	Gln	Thr	Pro	Glu	Leu	Lys	Gly	Asn	Lys	Leu	Leu	115	120	125
Val	Val	Ala	Arg	His	Glu	Ala	Glu	Ala	Leu	Ala	Ile	Lys	Arg	Arg	Phe	130	135	140
Ala	Lys	Lys	Ile	Ala	Asp	Val	Tyr	Ala	Ser	Phe	Gly	Phe	Pro	Pro	Leu	145	150	155
Gln	Leu	Asp	Val	Ser	Val	Glu	Pro	Ser	Lys	Gln	Glu	Met	Glu	Gln	Phe	165	170	175
Leu	Ala	Gln	Lys	Gln	Gln	Glu	Asp	Glu	Glu	Arg	Ala	Leu	Ala	Val	Leu	180	185	190
Thr	Asp	Leu	Ala	Arg	Glu	Glu	Glu	Lys	Ala	Ala	Ser	Ala	Pro	Pro	Ser	195	200	205
Gly	Pro	Leu	Val	Ile	Gly	Tyr	Pro	Ile	Arg	Asp	Glu	Glu	Pro	Val	Arg	210	215	220
Arg	Leu	Glu	Thr	Ile	Val	Glu	Glu	Glu	Arg	Arg	Val	Val	Val	Gln	Gly	225	230	235
Tyr	Val	Phe	Asp	Ala	Glu	Val	Ser	Glu	Leu	Lys	Ser	Gly	Arg	Thr	Leu	245	250	255
Leu	Thr	Met	Lys	Ile	Thr	Asp	Tyr	Thr	Asn	Ser	Ile	Leu	Val	Lys	Met	260	265	270
Phe	Ser	Arg	Asp	Lys	Glu	Asp	Ala	Glu	Leu	Met	Ser	Gly	Val	Lys	Lys	275	280	285
Gly	Met	Trp	Val	Lys	Val	Arg	Gly	Ser	Val	Gln	Asn	Asp	Thr	Phe	Val	290	295	300
Arg	Asp	Leu	Val	Ile	Ile	Ala	Asn	Asp	Leu	Asn	Glu	Ile	Ala	Ala	Asn	305	310	315
Glu	Arg	Gln	Asp	Thr	Ala	Pro	Glu	Gly	Glu	Lys	Arg	Val	Glu	Leu	His	325	330	335
Leu	His	Thr	Pro	Met	Ser	Gln	Met	Asp	Ala	Val	Thr	Ser	Val	Thr	Lys	340	345	350
Leu	Ile	Glu	Gln	Ala	Lys	Lys	Trp	Gly	His	Pro	Ala	Ile	Ala	Val	Thr	355	360	365

Asp His Ala Val Val Gln Ser Phe Pro Glu Ala Tyr Ser Ala Ala Lys
 370 375 380
 Lys His Gly Met Lys Val Ile Tyr Gly Leu Glu Ala Asn Ile Val Asp
 385 390 395 400
 Asp Gly Val Pro Ile Ala Tyr Asn Glu Thr His Arg Arg Leu Ser Glu
 405 410 415
 Glu Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val
 420 425 430
 Tyr Asn Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Asp Gly Glu
 435 440 445
 Ile Ile Asp Arg Phe Met Ser Phe Ala Asn Pro Gly His Pro Leu Ser
 450 455 460
 Val Thr Thr Met Glu Leu Thr Gly Ile Thr Asp Glu Met Val Lys Asp
 465 470 475 480
 Ala Pro Lys Pro Asp Glu Val Leu Ala Arg Phe Val Asp Trp Ala Gly
 485 490 495
 Asp Ala Thr Leu Val Ala His Asn Ala Ser Phe Asp Ile Gly Phe Leu
 500 505 510
 Asn Ala Gly Leu Ala Arg Met Gly Arg Gly Lys Ile Ala Asn Pro Val
 515 520 525
 Ile Asp Thr Leu Glu Leu Ala Arg Phe Leu Tyr Pro Asp Leu Lys Asn
 530 535 540
 His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
 545 550 555 560
 His His Arg Ala Ile Tyr Asp Ala Glu Ala Thr Gly His Leu Leu Met
 565 570 575
 Arg Leu Leu Lys Glu Ala Glu Glu Arg Gly Ile Leu Phe His Asp Glu
 580 585 590
 Leu Asn Ser Arg Thr His Ser Glu Ala Ser Tyr Arg Leu Ala Arg Pro
 595 600 605
 Phe His Val Thr Leu Leu Ala Gln Asn Glu Thr Gly Leu Lys Asn Leu
 610 615 620

Phe	Lys	Leu	Val	Ser	Leu	Ser	His	Ile	Gln	Tyr	Phe	His	Arg	Val	Pro	625	630	635	640
Arg	Ile	Pro	Arg	Ser	Val	Leu	Val	Lys	His	Arg	Asp	Gly	Leu	Leu	Val	645	650	655	
Gly	Ser	Gly	Cys	Asp	Lys	Gly	Glu	Leu	Phe	Asp	Asn	Leu	Ile	Gln	Lys	660	665	670	
Ala	Pro	Glu	Glu	Val	Glu	Asp	Ile	Ala	Arg	Phe	Tyr	Asp	Phe	Leu	Glu	675	680	685	
Val	His	Pro	Pro	Asp	Val	Tyr	Lys	Pro	Leu	Ile	Glu	Met	Asp	Tyr	Val	690	695	700	
Lys	Asp	Glu	Glu	Met	Ile	Lys	Asn	Ile	Ile	Arg	Ser	Ile	Val	Ala	Leu	705	710	715	720
Gly	Glu	Lys	Leu	Asp	Ile	Pro	Val	Val	Ala	Thr	Gly	Asn	Val	His	Tyr	725	730	735	
Leu	Asn	Pro	Glu	Asp	Lys	Ile	Tyr	Arg	Lys	Ile	Leu	Ile	His	Ser	Gln	740	745	750	
Gly	Gly	Ala	Asn	Pro	Leu	Asn	Arg	His	Glu	Leu	Pro	Asp	Val	Tyr	Phe	755	760	765	
Arg	Thr	Thr	Asn	Glu	Met	Leu	Asp	Cys	Phe	Ser	Phe	Leu	Gly	Pro	Glu	770	775	780	
Lys	Ala	Lys	Glu	Ile	Val	Val	Asp	Asn	Thr	Gln	Lys	Ile	Ala	Ser	Leu	785	790	795	800
Ile	Gly	Asp	Val	Lys	Pro	Ile	Lys	Asp	Glu	Leu	Tyr	Thr	Pro	Arg	Ile	805	810	815	
Glu	Gly	Ala	Asp	Glu	Glu	Ile	Arg	Glu	Met	Ser	Tyr	Arg	Arg	Ala	Lys	820	825	830	
Glu	Ile	Tyr	Gly	Asp	Pro	Leu	Pro	Lys	Leu	Val	Glu	Glu	Arg	Leu	Glu	835	840	845	
Lys	Glu	Leu	Lys	Ser	Ile	Ile	Gly	His	Gly	Phe	Ala	Val	Ile	Tyr	Leu	850	855	860	
Ile	Ser	His	Lys	Leu	Val	Lys	Lys	Ser	Leu	Asp	Asp	Gly	Tyr	Leu	Val	865	870	875	880

Gly Ser Arg Gly Ser Val Gly Ser Ser Phe Val Ala Thr Met Thr Glu
 885 890 895
 Ile Thr Glu Val Asn Pro Leu Pro Pro His Tyr Val Cys Pro Asn Cys
 900 905 910
 Lys His Ser Glu Phe Phe Asn Asp Gly Ser Val Gly Ser Gly Phe Asp
 915 920 925
 Leu Pro Asp Lys Asn Cys Pro Arg Cys Gly Thr Lys Tyr Lys Lys Asp
 930 935 940
 Gly His Asp Ile Pro Phe Glu Thr Phe Leu Gly Phe Lys Gly Asp Lys
 945 950 955 960
 Val Pro Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Pro Arg Ala
 965 970 975
 His Asn Tyr Thr Lys Val Leu Phe Gly Glu Asp Asn Val Tyr Arg Ala
 980 985 990
 Gly Thr Ile Gly Thr Val Ala Asp Lys Thr Ala Tyr Gly Phe Val Lys
 995 1000 1005
 Ala Tyr Ala Ser Asp His Asn Leu Glu Leu Arg Gly Ala Glu Ile Asp
 1010 1015 1020
 Leu Ala Ala Gly Cys Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro
 1025 1030 1035 1040
 Gly Gly Ile Ile Val Val Pro Asp Tyr Met Glu Ile Tyr Asp Phe Thr
 1045 1050 1055
 Pro Ile Gln Tyr Pro Ala Asp Asp Thr Ser Ser Glu Trp Arg Thr Thr
 1060 1065 1070
 His Phe Asp Phe His Ser Ile His Asp Asn Leu Leu Lys Leu Asp Ile
 1075 1080 1085
 Leu Gly His Asp Asp Pro Thr Val Ile Arg Met Leu Gln Asp Leu Ser
 1090 1095 1100
 Gly Ile Asp Pro Lys Thr Ile Pro Thr Asp Asp Pro Asp Val Met Gly
 1105 1110 1115 1120
 Ile Phe Ser Ser Thr Glu Pro Leu Gly Val Thr Pro Glu Gln Ile Met
 1125 1130 1135

Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val
 1140 1145 1150
 Arg Gln Met Leu Glu Glu Thr Arg Pro Lys Thr Phe Ser Glu Leu Val
 1155 1160 1165
 Gln Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Gly Asn Ala
 1170 1175 1180
 Gln Glu Leu Ile Gln Asn Gly Thr Cys Thr Leu Ser Glu Val Ile Gly
 1185 1190 1195 1200
 Cys Arg Asp Asp Ile Met Val Tyr Leu Ile Tyr Arg Gly Leu Glu Pro
 1205 1210 1215
 Ser Leu Ala Phe Lys Ile Met Glu Ser Val Arg Lys Gly Lys Gly Leu
 1220 1225 1230
 Thr Pro Glu Phe Glu Ala Glu Met Arg Lys His Asp Val Pro Glu Trp
 1235 1240 1245
 Tyr Ile Asp Ser Cys Lys Lys Ile Lys Tyr Met Phe Pro Lys Ala His
 1250 1255 1260
 Ala Ala Ala Tyr Val Leu Met Ala Val Arg Ile Ala Tyr Phe Lys Val
 1265 1270 1275 1280
 His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu
 1285 1290 1295
 Asp Phe Asp Leu Asp Ala Met Ile Lys Gly Ser Pro Ala Ile Arg Lys
 1300 1305 1310
 Arg Ile Glu Glu Ile Asn Ala Lys Gly Ile Gln Ala Thr Ala Lys Glu
 1315 1320 1325
 Lys Ser Leu Leu Thr Val Leu Glu Val Ala Leu Glu Met Cys Glu Arg
 1330 1335 1340
 Gly Phe Ser Phe Lys Asn Ile Asp Leu Tyr Arg Ser Gln Ala Thr Glu
 1345 1350 1355 1360
 Phe Val Ile Asp Gly Asn Ser Leu Ile Pro Pro Phe Asn Ala Ile Pro
 1365 1370 1375
 Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu
 1380 1385 1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser
1395 1400 1405

Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu
1410 1415 1420

Pro Asp His Asn Gln Leu Ser Leu Phe
1425 1430

<210> 185
<211> 199
<212> PRT
<213> *Thermus thermophilus*

<400> 185
Thr Pro Lys Gly Lys Asp Leu Val Arg His Leu Glu Asn Arg Ala Lys
1 5 10 15

Arg Leu Gly Leu Arg Leu Pro Gly Gly Val Ala Gln Tyr Leu Ala Ser
20 25 30

Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala
35 40 45

Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala
50 55 60

Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu
65 70 75 80

Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu
85 90 95

Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala
100 105 110

Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys
115 120 125

Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys
130 135 140

Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu
145 150 155 160

Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys

165

170

175

Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro
 180 185 190

Ala Gly Gln Pro Arg Val Asp
 195

<210> 186

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 186

gcccgatacc tcgctccct cgagggg

27

<210> 187

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 187

ggcccccttg gccttctcgg cctccat

27

<210> 188

<211> 331

<212> DNA

<213> Thermus thermophilus

<400> 188

agactcgagg ccctggagcg ggagctggag aagcttgccc tcctctcccc acccctcacc 60
 ctggagaagg tggagaaggt ggtggccctg aggccccccc tcacgggctt tgacctggtg 120
 cgctccgtcc tggagaagga cccaaggag gccctcctgc gcctcaggcg cctcaggagg 180
 gagggggagg agccctcag gctcctcggg gccctctcct ggcagttcgc cctcctcgcc 240
 cgggccttct tcctcctcgg ggaaaacccc aggcccaagg aggaggacct cgcccgctc 300
 gagggcccacc cctacgccgc caagaaggcc a 331

<210> 189

<211> 110
 <212> PRT
 <213> Thermus thermophilus

<400> 189
 Arg Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala Leu Leu Ser
 1 5 10 15
 Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala Leu Arg Pro
 20 25 30
 Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu Lys Asp Pro
 35 40 45
 Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu
 50 55 60
 Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala
 65 70 75 80
 Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp
 85 90 95
 Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala
 100 105 110

<210> 190
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 190
 gtggtgtcta gacatcataa cggttctggc a

31

<210> 191
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 191

gagggccacc accttctcca ccttctc 27

<210> 192
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 192
 ctccgtcctg gagaaggacc ccaag 25

<210> 193
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<220>
 <221> primer_bind
 <222> (15)
 <223> S at position 15 can be either C or G

<220>
 <221> primer_bind
 <222> (27)
 <223> S at position 27 can be either C or G

<400> 193
 cgcgaattca acgcsctcct caagacsct 29

<210> 194
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 194
 gacacttaac atatggcat cgccttcacc g 31

<210> 195
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 195
gtgtgtgaat tcgggtcaac gggcgaggcg gaggaccg

38

<210> 196
<211> 10
<212> PRT
<213> *Deinococcus radiodurans*

<400> 196
Val Ile Leu Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 197
<211> 10
<212> PRT
<213> *Methanococcus jannaschii*

<400> 197
Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 198
<211> 10
<212> PRT
<213> *Thermotoga maritima*

<400> 198
Leu Val Leu Asn Pro Gly Ser Ala Gly Arg
1 5 10

<210> 199
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 199

ctggtgaacc cgggctccgt gggccagc

28

<210> 200

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 200

Leu Leu Val Asn Pro Gly Ser Val Gly Gln

1

5

10

<210> 201

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 201

ctcgaggagc ttgaggaggg tgttggc

27

<210> 202

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 202

Ala Asn Thr Leu Leu Lys Leu Leu Glu

1

5

<210> 203

<211> 32

<212> PRT

<213> *Deinococcus radiodurans*

<400> 203

Gly Phe Gly Gly Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly
20 25 30

<210> 204

<211> 32

<212> PRT

<213> *Caenorhabditis elegans*

<400> 204

Gly Phe Asp Gly Ile Gln Leu His Gly Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly
20 25 30

<210> 205

<211> 32

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 205

Gly Phe Ser Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly
20 25 30

<210> 206

<211> 32

<212> PRT

<213> Archaeoglobus fulgidus

<400> 206

Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly
20 25 30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 207

catcctggac tcggcccacc tcctcaccga 30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 208

Ile Leu Asp Ser Ala His Leu Leu Thr
1 5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 209

gaggaggtag ccgtgggccg cgtggagctc cac 33

<210> 210
 <211> 11
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: polypeptide

 <400> 210
 Val Glu Leu His Ala Ala His Gly Tyr Leu Leu
 1 5 10

<210> 211
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

<400> 211
 ggctttccca tatggctcta caccggctc ac 32

<210> 212
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

<400> 212
 gcgtggatcc acggtcatgt ctctaagtc 29